

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 16:56:17 ; Search time 69 Seconds
(without alignments)

Title: US-09-784-423-32

reflect score: 1000
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Scoring table: OLIGO NUC

gapup 60.0 , gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters:	1139956
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	51	5.1	658	3	US-08-999-416-595	Sequence 595, App
3	50	5.0	11282	4	US-09-754-250-3	Sequence 3, Appl
4	47	4.7	1947	2	US-08-989-925-2	Sequence 2, Appl
C 5	47	4.7	6804	4	US-09-740-041-3	Sequence 3, Appl
6	46	4.6	17000	4	US-09-679-298A-18	Sequence 18, Appl
C 7	46	4.6	90541	4	US-09-679-359A-3	Sequence 3, Appl
C 8	45	4.5	43950	4	US-09-735-334A-3	Sequence 3, Appl
9	45	4.5	43950	4	US-10-060-332-3	Sequence 3, Appl
C 10	45	4.5	70000	4	US-09-851-896-3	Sequence 3, Appl
11	44	4.4	3609	4	US-09-705-299-11	Sequence 11, Appl
C 12	44	4.4	9862	4	US-09-691-861A-3	Sequence 3, Appl
C 13	44	4.4	55298	4	US-09-491-356C-1	Sequence 1, Appl
14	44	4.4	53065	4	US-09-813-817-3	Sequence 3, Appl
C 15	44	4.4	53065	4	US-09-813-817-3	Sequence 3, Appl
16	44	4.4	53065	4	US-09-978-197-3	Sequence 3, Appl
C 17	44	4.4	53065	4	US-09-978-197-3	Sequence 3, Appl
18	44	4.4	64467	4	US-09-803-671B-3	Sequence 3, Appl
C 19	44	4.4	87350	3	US-08-781-891-79	Sequence 3, Appl
C 20	44	4.4	87350	4	US-09-618-166-79	Sequence 79, Appl
C 21	44	4.4	87543	4	US-09-791-211-3	Sequence 79, Appl
22	43	4.3	1001	4	US-09-671-317-258	Sequence 3, Appl
C 23	43	4.3	1001	4	US-09-671-317-259	Sequence 258, App
24	43	4.3	1001	4	US-09-671-317-260	Sequence 259, App
C 25	43	4.3	2598	4	US-09-671-317-260	Sequence 260, App
26	43	4.3	2598	4	US-09-593-995-10	Sequence 10, Appl
C 26	43	4.3	21234	4	US-09-810-671-3	Sequence 3, Appl
C 27	43	4.3	46718	4	US-09-816-093-3	Sequence 3, Appl

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Best Local Similarity	100.0%;	Pred. No. 0;		

C	28	43	4.3	74962	4	US-09-695-853A-3	Sequence 3, Appl.
C	29	43	4.3	84495	4	US-03-797-906-3	Sequence 3, Appl.
C	30	42	4.2	2582	1	US-08-441-370-1	Sequence 1, Appl.
C	31	42	4.2	2784	1	US-08-471-454-1	Sequence 1, Appl.
C	32	42	4.2	2784	2	US-08-466-974-1	Sequence 1, Appl.
C	33	42	4.2	2784	2	US-08-471-453-1	Sequence 1, Appl.
C	34	42	4.2	3441	4	US-09-026-033-17	Sequence 17, Appl.
C	35	42	4.2	3451	4	US-09-611-286-1	Sequence 1, Appl.
C	36	42	4.2	90541	4	US-09-759-359A-3	Sequence 3, Appl.
C	37	42	4.2	162450	4	US-09-345-883-1	Sequence 1, Appl.
C	38	41	4.1	1094	4	US-09-205-258-2	Sequence 2, Appl.
C	39	41	4.1	1110	4	US-09-511-625B-43	Sequence 43, Appl.
C	40	41	4.1	1437	6	5187077-16	Patent No. 5187077
C	41	41	4.1	1437	6	5427925-14	Patent No. 5427925
C	42	41	4.1	1554	1	US-08-370-975B-10	Sequence 10, Appl.
C	43	41	4.1	1701	3	US-09-078-294-9	Sequence 9, Appl.
C	44	41	4.1	6330	4	US-09-880-427-2	Sequence 2, Appl.
C	45	41	4.1	6330	4	US-09-306-536B-2	Sequence 2, Appl.

ALIGNMENTS

```

RESULT 1
US-09-018-584A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffrey W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Promega Corporation
 STREET: 2800 Woods Hollow Road
 CITY: Madison
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53711-5399
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
 COMPUTER: IBM compatible PC
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Word 97 (DOS text format)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/018,584A
 FILING DATE: 04-Feb-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Grady J. Frenchick
 REGISTRATION NUMBER: 29,018
 REFERENCE/DOCKET NUMBER: 16026,9180
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 257-3501
 TELEFAX: (608) 257-2275
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:

LENGTH: 1000 bp
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Circular
 MOLECULE TYPE: Genomic DNA
 HYPOTHETICAL: no
 IMMEDIATE SOURCE:
 CLONE: S132
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 22
 US-09-018-584A-12

Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGTGACCTTATCTCTCTGAACCTCAGTTCCTCATCGTAAATGAAGCTGCTAG 60
Db |||||
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Db |||||
Qy 61 ATTGTTGTAATAAATAAATAAATGAATAGCTAGGCGGCTGCTCAGCGCTGTATCCCA 120
Db |||||
Qy 61 ATTGTTGTAATAAATAAATAAATGAATAGCTAGGCGGCTGCTCAGCGCTGTATCCCA 120
Db |||||
Qy 121 GCATCTTAGAGGTGGAAGGCTGATCCTAGTGGTCAAGCTGCTGAGCAGCGCTG 180
Db |||||
Qy 121 GCATCTTAGAGGTGGAAGGCTGATCCTAGTGGTCAAGCTGCTGAGCAGCGCTG 180
Db |||||
Qy 181 GCCAACACGGTGAACCCCATCTCTCTAAATAAATAAATAAATAGCTGGTGGCT 240
Db |||||
Qy 181 GCCAACACGGTGAACCCCATCTCTCTAAATAAATAAATAAATAGCTGGTGGCT 240
Db |||||
Qy 241 CACACCTGTAAATCCCGACCTTTGGGAGGCTGAGACGGGTGGATCAGCTGAAGTCAGGAG 300
Db |||||
Qy 241 CACACCTGTAAATCCCGACCTTTGGGAGGCTGAGACGGGTGGATCAGCTGAAGTCAGGAG 300
Db |||||
Qy 301 TTCAAGCCGAGCTGGGCAACATGCTGAAACCATCTCTCTAAATAAATAAATAAATAG 360
Db |||||
Qy 301 TTCAAGCCGAGCTGGGCAACATGCTGAAACCATCTCTCTAAATAAATAAATAAATAG 360
Db |||||
Qy 361 CCAGGTGTGGTGGCACAGCCTGTAGTCCAGCTACTTTGGAGGCTGAGGCGGAAGATC 420
Db |||||
Qy 361 CCAGGTGTGGTGGCACAGCCTGTAGTCCAGCTACTTTGGAGGCTGAGGCGGAAGATC 420
Db |||||
Qy 421 GCTTGAACCGAGTGGGAGGCTGAGTGGAGCGGAGATAGAGTCACTGCTCCAGCC 480
Db |||||
Qy 421 GCTTGAACCGAGTGGGAGGCTGAGTGGAGCGGAGATAGAGTCACTGCTCCAGCC 480
Db |||||
Qy 481 TGCGTACAGAGCAAGCTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
Db |||||
Qy 481 TGCGTACAGAGCAAGCTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
Db |||||
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Db |||||
Qy 541 AATAAATAAATAAATAAATAAAGGCTGGCACTTTGCCCTAGCACTTATATGCCAATA 600
Db |||||
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Db |||||
Qy 601 AGTAAATAGCTATCAATATCCCAACCCCTACCACTGTGCTGAAATTTAGTTTCTTGTG 660
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Qy 661 ACCCCCATTTAGACTTAAGCAGATTTCTCAGCTGCTCTCTGTAATTTCTGCTGCT 720
Db |||||
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Db |||||
Qy 721 GGCATATAGTGGTCTCAGTGAACATGCTGAGTGAATGAGCAATGCAAGGAATCTCC 780
Db |||||
Qy 721 GGCATATAGTGGTCTCAGTGAACATGCTGAGTGAATGAGCAATGCAAGGAATCTCC 780
Db |||||
Qy 781 AGGCCATCTGGAGCCCTCCCGAGCGGTGAGTTGCGGAATCTCATAGTCTGCTCAAT 840
Db |||||
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Db |||||
Qy 841 GGCCCACTGAAAGGTAGAGAGTTCTGGGTCCACCTCCGACCCCTCTCTGCTGCTC 900
Db |||||
Qy 841 GGCCCACTGAAAGGTAGAGAGTTCTGGGTCCACCTCCGACCCCTCTCTGCTGCTC 900
Db |||||
Qy 901 TGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
Db |||||
Qy 961 CAGACTGCAAGGAGCCGAGCAATGATGACCGGCTGC 1000
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Db |||||

RESULT 2

US-08-998-416-595/c

; Sequence 595, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHEYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/POCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 595:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1408RP
; US-08-998-416-595

Query Match 5.1%; Score 51; DB 3; Length 658;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 655 GAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 605
Db |||||

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US-09-754-250-3
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0


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; Patent No. 6482935
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000892
; CURRENT APPLICATION NUMBER: US/09/691,861A
; CURRENT FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-861A-3

Query Match      4.4%; Score 44; DB 4; Length 9862;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 TGGTGGCACAGCCTGTAGTCCAGCTACTTGGAGGCTGAGGC 411
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Db 4344 TGGTGGCACAGCCTGTAGTCCAGCTACTTGGAGGCTGAGGC 4301

RESULT 13
US-09-491-356C-1/c
; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisl, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 55298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (838)..(838)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (16728)..(16728)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22750)..(22750)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (22756)..(22756)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (28519)..(28519)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (44804)..(44804)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc feature
; LOCATION: (45002)..(45002)
; OTHER INFORMATION: n is not determined
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; NAME/KEY: misc feature
; LOCATION: (54049)..(54049)
; OTHER INFORMATION: n is not determined
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; LOCATION: (54226)..(54226)
; OTHER INFORMATION: n is not determined
US-09-491-356C-1

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Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-813-817-3
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

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Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAATAATACAAAATTAGCCAGGTGTGGTGCCACA 377
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Db 58882 CGTCTCTACTAAATAATACAAAATTAGCCAGGTGTGGTGCCACA 58925

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US-09-813-817-3/c
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match      4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 555
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Db 3447 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 3404
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Search completed: January 31, 2004, 17:27:16
Job time : 72 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:07:51 ; Search time 352 Seconds
(without alignments)
10353.854 Million cell updates/sec

Title: US-09-784-423-32

Perfect score: 1000

Sequence: 1 GTGTGACCTATCCCTCT.....CAGATGATGACCGGCGTGC 1000

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Word size : 0

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	58	5.8	11627	11	Sequence 32, Appl
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4	55	5.5	677	14	Sequence 134421
5	55	5.5	2635	12	Sequence 134421
6	55	5.5	43183	12	Sequence 1607, Ap
7	54	5.4	439	12	Sequence 28, Appl
8	54	5.4	593	13	Sequence 7130, Ap
9	53	5.3	307	12	Sequence 627, App
10	53	5.3	650	13	Sequence 634, App
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12	52	5.2	431	13	Sequence 239196
13	52	5.2	431	14	Sequence 278501
14	52	5.2	432	13	Sequence 278501
15	52	5.2	432	14	Sequence 266549

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52	5.2	797	14	US-10-027-632-127789	Sequence 127789,
52	5.2	2701	10	US-09-764-877-3378	Sequence 3378, Ap
52	5.2	2701	12	US-10-242-515-3378	Sequence 3378, Ap
52	5.2	1503841	9	US-09-795-686-1	Sequence 1, Appli
52	5.2	1503841	9	US-09-795-686-1	Sequence 1, Appli
52	5.2	1503841	10	US-09-946-807-1	Sequence 1, Appli
52	5.1	739	13	US-10-027-632-131328	Sequence 131328,
52	5.1	739	14	US-10-027-632-131328	Sequence 131328,
52	5.1	761	13	US-10-027-632-131329	Sequence 131329,
52	5.1	761	13	US-10-027-632-131329	Sequence 131329,
52	5.1	761	14	US-10-027-632-131330	Sequence 149274,
52	5.1	761	14	US-10-027-632-149274	Sequence 149274,
52	5.1	768	13	US-10-027-632-171996	Sequence 171996,
52	5.1	768	14	US-10-027-632-171996	Sequence 171996,
52	5.1	43419	12	US-10-292-798-1451	Sequence 1451, Ap
52	5.1	43419	13	US-10-017-161-1795	Sequence 1795, Ap
52	5.0	276	9	US-09-764-869-2086	Sequence 2086, Ap
52	5.0	276	12	US-10-227-577-2086	Sequence 2086, Ap
52	5.0	276	15	US-10-091-504-2086	Sequence 2086, Ap
52	5.0	337	12	US-10-242-535A-39971	Sequence 39971, A
52	5.0	496	13	US-10-027-632-314826	Sequence 314826,
52	5.0	496	14	US-10-027-632-314826	Sequence 314826,
52	5.0	505	13	US-10-027-632-68196	Sequence 68196, A
52	5.0	505	13	US-10-027-632-68756	Sequence 68756, A
52	5.0	505	13	US-10-027-632-68968	Sequence 68968, A
52	5.0	505	14	US-10-027-632-68196	Sequence 68196, A
52	5.0	505	14	US-10-027-632-68756	Sequence 68756, A

ALIGNMENTS

RESULT 1

US-09-784-423-32

Sequence 32, Application US/09784423

Patent No. US20020012924A1

GENERAL INFORMATION:

APPLICANT: Schumm, James W.

Bacher, Jeffery W.

TITLE OF INVENTION: IDENTIFYING AND METHODS FOR

REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Promega Corporation

STREET: 2800 Woods Hollow Road

CITY: Madison

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53711-5399

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

COMPUTER: IBM compatible PC

OPERATING SYSTEM: Windows 95

SOFTWARE: Word 97 (DOS text format)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784,423

FILING DATE: 15-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/018,584

FILING DATE: 04-Feb-1998

ATTORNEY/AGENT INFORMATION:

NAME: Grady J. Frenchick

REGISTRATION NUMBER: 29,018

REFERENCE/DOCKET NUMBER: 16026.9180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 257-3501

TELEFAX: (608) 257-2275

INFORMATION FOR SEQ ID NO: 32

US-10-027-632-134421

Query Match 5.5%; Score 55; DB 13; Length 677;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 TAAATAACAAAATTAGCCAGGTGTGGTGGCACAGCCTGTAGTCCAGCTACT 397
Db 341 TAAATAACAAAATTAGCCAGGTGTGGTGGCACAGCCTGTAGTCCAGCTACT 287

RESULT 4

US-10-027-632-134421/c
; Sequence 134421, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134421
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134421

Query Match 5.5%; Score 55; DB 14; Length 677;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 TAAATAACAAAATTAGCCAGGTGTGGTGGCACAGCCTGTAGTCCAGCTACT 397
Db 341 TAAATAACAAAATTAGCCAGGTGTGGTGGCACAGCCTGTAGTCCAGCTACT 287

RESULT 5

US-10-104-047-1607/c
; Sequence 1607, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1607
; LENGTH: 2635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1607

Query Match 5.5%; Score 55; DB 12; Length 2635;

Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 318 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAATAGCCAGGTGTGGTG 372
Db 2019 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAATAGCCAGGTGTGGTG 1965

RESULT 6

US-10-085-117-28
; Sequence 28, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 05/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 43183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-28

Query Match 5.5%; Score 55; DB 12; Length 43183;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 318 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAATAGCCAGGTGTGGTG 372
Db 30963 CAACATGGTGAACACCGCTCTCTACTTAAATAATACAAAATAGCCAGGTGTGGTG 31017

RESULT 7

US-10-242-535A-7130
; Sequence 7130, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C. C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7130
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-7130

Query Match 5.4%; Score 54; DB 12; Length 439;
Best Local Similarity 100.0%; Pred. No. 6.3e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 GGGTGGCGGTGCTCACACCTGTATATCCAGCATTTCGGAGGCTGAGAGCGGTG 281
Db 219 GGGTGGCGGTGCTCACACCTGTATATCCAGCATTTCGGAGGCTGAGAGCGGTG 272

RESULT 8

US-10-012-697-627
; Sequence 627, Application US/10012697
; Publication No. US20030215803A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Dmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Dmanac, Srejana
; APPLICANT: Labat, Ivan
; APPLICANT: Leebkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: US/10/012,697
; CURRENT FILING DATE: 2003-01-21
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/254,648
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/275,668
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 1568
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 627
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 394, 404, 409, 411, 426, 432, 477, 499, 508, 525, 527, 539,
; LOCATION: 549, 555, 567, 592
; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-627

Query Match 5.4%; Score 54; DB 13; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTGGGGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGCGGTG 281

DB 94 GGTGGGGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGCGGTG 147

RESULT 9

US-10-074-024-634
; Sequence 634, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC001C1
; CURRENT APPLICATION NUMBER: US/10/074,024
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-024-634

Query Match 5.3%; Score 53; DB 12; Length 307;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGCGGTGATCA 286

DB 14 GGTGGCTCACACCTGTAATCCAGCATTGGAGGCTTGAGCGGTGATCA 66

RESULT 10

US-10-027-632-239196/c
; Sequence 239196, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239196
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(650)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-239196

Query Match 5.3%; Score 53; DB 13; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 558

DB 254 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 202

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RESULT 11
US-10-027-632-239196/c
; Sequence 239196, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239196
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(650)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-239196

Query Match          5.3%; Score 53; DB 14; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
Db 254 CAGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 202

RESULT 12
US-10-027-632-278501/c
; Sequence 278501, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278501
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-278501

Query Match          5.3%; Score 53; DB 14; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
Db 254 CAGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 202
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US-10-027-632-278501/c
; Sequence 278501, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278501
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-278501

Query Match          5.2%; Score 52; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACCGCTGTAGT 387
Db 376 TCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACCGCTGTAGT 325

RESULT 13
US-10-027-632-278501/c
; Sequence 278501, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278501
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-278501

Query Match          5.2%; Score 52; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACCGCTGTAGT 387
Db 376 TCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGGCACACCGCTGTAGT 325

RESULT 14
US-10-027-632-266549/c
; Sequence 266549, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
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/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 266549
/ LENGTH: 432
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-266549
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Query Match      5.2% Score 52; DB 13; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGTGGCACACGCGCTGTAGT 387
Db 376 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGTGGCACACGCGCTGTAGT 325
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RESULT 15

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US-10-027-632-266549/c
/ Sequence 266549, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 266549
/ LENGTH: 432
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-266549
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Query Match      5.2% Score 52; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGTGGCACACGCGCTGTAGT 387
Db 376 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGTGGCACACGCGCTGTAGT 325
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Search completed: January 31, 2004, 17:33:22
Job time : 356 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 15:28:31 ; Search time 90 Seconds
(without alignments)
4904.257 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GGTGTGACCTTATCCCTCTCT.....CAGATGATGACCGGCGTGC 1000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	999	99.9	1000	3	US-09-018-584A-32
2	296	29.6	15297	4	US-09-817-180-3
3	284	28.4	2713	2	US-08-915-901-6
4	284	28.4	2713	4	US-09-154-602-6
5	284	28.4	7720	3	US-09-318-448-5
6	279.6	28.0	53332	4	US-09-801-861-3
7	277.8	27.8	7210	2	US-08-257-963B-10
8	277.8	27.8	7210	4	US-08-367-841A-10
9	277.8	27.8	7210	5	PCT-US95-07201-10
10	277.8	27.8	14581	4	US-08-520-373D-4
11	277.8	27.8	22481	4	US-08-367-841A-43
12	277.8	27.8	22481	5	PCT-US95-07201-43
13	277.8	27.8	22484	4	US-09-875-223-2
14	275.6	27.6	112132	4	US-09-741-150-3
15	272.6	27.3	29629	4	US-09-729-995-3
16	271.4	27.1	62804	4	US-09-800-960-3
17	269.6	27.0	59085	4	US-09-813-817-3
18	269.6	27.0	59085	4	US-09-740-041-3
19	268	26.8	66804	4	US-09-740-041-3
20	267.4	26.7	14581	4	US-08-520-373D-4
21	266.6	26.7	17377	1	US-07-906-871-15
22	265.8	26.6	7210	2	US-08-257-963B-10
23	265.8	26.6	7210	4	US-08-367-841A-10
24	265.8	26.6	7210	5	PCT-US95-07201-10
25	265.8	26.6	22481	4	US-08-367-841A-43
26	265.8	26.6	22481	5	PCT-US95-07201-43
27	265.8	26.6	22484	4	US-09-875-223-2

Sequence 3, Appli
Sequence 17, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 258, App
Sequence 259, App
Sequence 250, App
Sequence 1, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-09-018-584A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA: US/09/018,584A
; APPLICATION NUMBER: 04-Feb-1998
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: SL32
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; US-09-018-584A-32

Query Match 99.9%; Score 999; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 3.7e-217;

Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGTGACCTTATCTCTCTGAACTCAGTTCCTCATCCGTAAATGAAAGCTGTAG 60
Db |||||
Qy 1 GGTGTGACCTTATCTCTCTGAACTCAGTTCCTCATCCGTAAATGAAAGCTGTAG 60
Db |||||
Qy 61 ATTCTTTGTAATAAATTAATATGAAATAGGCTAGGCGGGTGCATCCGCTGTAATCCCA 120
Db |||||
Qy 61 ATTCTTTGTAATAAATTAATATGAAATAGGCTAGGCGGGTGCATCCGCTGTAATCCCA 120
Db |||||
Qy 121 GCATTTAGAGGTGCAAGAGGTTGATCATCTTGAAGTTCAGAGGTTTTCAGACAGCCTG 180
Db |||||
Qy 121 GCATTTAGAGGTGCAAGAGGTTGATCATCTTGAAGTTCAGAGGTTTTCAGACAGCCTG 180
Db |||||
Qy 181 GCCAACACGCTGAAACCCCATCTCTACTATAAATAAATAAATAGCTNGGCTGGCT 240
Db |||||
Qy 181 GCCAACACGCTGAAACCCCATCTCTACTATAAATAAATAAATAGCTNGGCTGGCT 240
Db |||||
Qy 241 CACACCTGTAATCCCGACACTTTGGGAGGCTGAGACGGTGGATCACCTGAAGTCAGGAG 300
Db |||||
Qy 241 CACACCTGTAATCCCGACACTTTGGGAGGCTGAGACGGTGGATCACCTGAAGTCAGGAG 300
Db |||||
Qy 301 TTCAAGGCCAGGCTGGGCAACATGTTGAAACCCAGTCTCTACTATAAATAAATAAATAAATAG 360
Db |||||
Qy 301 TTCAAGGCCAGGCTGGGCAACATGTTGAAACCCAGTCTCTACTATAAATAAATAAATAAATAG 360
Db |||||
Qy 361 CCAGGTGTGGTGACACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCGGGAAGATC 420
Db |||||
Qy 361 CCAGGTGTGGTGACACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCGGGAAGATC 420
Db |||||
Qy 421 GCTTTGAACCCAGTGTAGGAGGTTGAGTGGAGGCTGAGGAGTCACTGACCTCCAGCC 480
Db |||||
Qy 421 GCTTTGAACCCAGTGTAGGAGGTTGAGTGGAGGCTGAGGAGTCACTGACCTCCAGCC 480
Db |||||
Qy 481 TGGGTGACAGAGCAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
Db |||||
Qy 481 TGGGTGACAGAGCAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
Db |||||
Qy 541 AATAAATAAATAAATAAATAAATAAAGGCTGGCACTTTGCTAGCACTTATATGCCCAATA 600
Db |||||
Qy 541 AATAAATAAATAAATAAATAAATAAAGGCTGGCACTTTGCTAGCACTTATATGCCCAATA 600
Db |||||
Qy 601 AGTAATAGCTATCAATATCCGACCCCTACCACTGCTGTAATTTAGTTCTTTTGTGTC 660
Db |||||
Qy 601 AGTAATAGCTATCAATATCCGACCCCTACCACTGCTGTAATTTAGTTCTTTTGTGTC 660
Db |||||
Qy 661 ACCCCCCATTAGACTTAAGGAGCAATTTCTACCGTACTCTCTGTAATTTCTGTTTCT 720
Db |||||
Qy 661 ACCCCCCATTAGACTTAAGGAGCAATTTCTACCGTACTCTCTGTAATTTCTGTTTCT 720
Db |||||
Qy 721 GGCACATAGTTGGGTCTCAGTGAACATGGTGAATGAGCAAAATGCAAGGAATCTCC 780
Db |||||
Qy 721 GGCACATAGTTGGGTCTCAGTGAACATGGTGAATGAGCAAAATGCAAGGAATCTCC 780
Db |||||
Qy 781 AGGCCATCTGGAGCCCTCCGAGCGGGTGAATTCGGGAACTCATAGCTGTCTCTCAAT 840
Db |||||
Qy 781 AGGCCATCTGGAGCCCTCCGAGCGGGTGAATTCGGGAACTCATAGCTGTCTCTCAAT 840
Db |||||
Qy 841 GGCCCACTGAAGAGGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTCTGACTCAC 900
Db |||||
Qy 841 GGCCCACTGAAGAGGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTCTGACTCAC 900
Db |||||
Qy 901 TGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
Db |||||
Qy 901 TGTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
Db |||||
Qy 961 CAGACTGCAAGAGGCCCCAGCAATGATGACCGGCTGC 1000
Db |||||
Qy 961 CAGACTGCAAGAGGCCCCAGCAATGATGACCGGCTGC 1000
Db |||||

RESULT 2
US-09-817-180-3

; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01183
; CURRENT APPLICATION NUMBER: US/09/817,180
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

Query Match 29.6%; Score 296; DB 4; Length 15297;
Best local Similarity 83.4%; Pred. No. 4.6e-58;
Matches 371; Conservative 0; Mismatches 71; Indels 3; Gaps 3;

Qy 97 CGGTGGCTCAGCGCTGTATCCAGACAGCTGGCCACACGCGTGAACCCCATCTCTACTAAAAATAA 216
Db 11700 CAGTTGTCTACGCGTGTATCCAGACAGCTGGGAGGCTGAGCTGGGTGATCACTTGAG 11759

Qy 157 GTCAAGAGTTTTCAGACAGCAGCTGGCCACACGCGTGAACCCCATCTCTACTAAAAATAA 216
Db 11760 CCCAGGAG-TTCAGATCAGTTGGACACACAGTGAACCTCCATCTGTACAAAAATAC 11818

Qy 217 AAAATTAGCTNGGGTGGCTGCCTACACCTGTAAATCCAGACACTTTGGGAGGCTGAGAC 276
Db 11819 AAAAATAGACTGGGACGCGTGGCTACACCTGTAAATCCAGACACTTTGGGAGGCGGAGC 11878

Qy 277 GGGTGGATCACTTGAAGTTCAGAGGTTCAAGGCGCCCTGGGCAACATGTTGAACCAAGT 336
Db 11879 AGGTGGATCACTTGGTGGTGGAGGTTGAGACCCAGCCAGCAACATGTTGAACCCCAT 11938

Qy 337 CTCTACTAAAAATACAAAAATTAGCCAGGTTGGTGGGACACCCCTGTAGTCCAGCTAC 396
Db 11939 CTCTACTAAAAATACAAAAATTAGCCAGGATGGTGGGACGCTGCTGTATCCAGCTAC 11998

Qy 397 TTGGAGGCTGAGGCGGAGAAATGCTTGAACCCAGTAGGAGGCTGAGGTTGAGTGGAGCCGA 456
Db 11999 TTGGAGGCTGAGGTTGGAGAAATGCTTGAACCCAGGAGGCGGAGGCTGAGTGGAGCCGA 12058

Qy 457 GATTAAGTCACTGCACTCCAGCTGGGTGAC-AGAGCAAGACTCCCTCTCAGAAAAATA 515
Db 12059 GAT-TGTGCACTGCACTCCAGCTGGGCGCAAGAGTGAACCTCCATCTCAAAAAAAC 12117

Qy 516 AATAAATAAATAAATAAATAAATAA 540
Db 12118 CAAAAACAAAAATACAAAAATA 12142

RESULT 3
US-08-916-901-6
; Sequence 6, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-901-6

Query March 28.4%; Score 284; DB 2; Length 2713;
Best Local Similarity 81.3%; Pred. No. 1.7e-55;
Matches 365; Conservative 0; Mismatches 81; Indels 3; Gaps 3;

QY 74 AATTAATGGAATAGGCTAGGCGGGTGGCTACGCGCTGTAATCCAGACACTTTAGAGG 133
DB 1688 AAAAAATCAAAATTTAGCGCGCGTGGTGGCTCACCTGTAATCCAGACTTTGGGAGG 1747
QY 134 TCGAAGAGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACGAGCTGGCCACACGGTGA 193
DB 1748 CTGAGCGAGGAGAAATCACTTGAGGTTCAGGAG-TTTGAGACCGAGCTGGCCACAGTGTGA 1806
QY 194 AACCCCATCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGTGGCTCACCTGTAATC 253
DB 1807 AACCTGTCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGAGGCGGGTGGCGCTGTAATC 1866
QY 254 CCAGACATTTGGGAGGCTGAGACGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACGAGCTGGCCACACGGTGA 313
DB 1867 TCAGACATTTGGGAGGCGGAGGAGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACGAGCTGGCCACAGCC 1926
QY 314 TGGGCAACATGGTGAACACCGTCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGTGG 373
DB 1927 TGGCCAAACATGGTGAACACCGCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGTGG 1986
QY 374 CACAGCGCTGTAGTCCAGCTACTTTGGAGGCTGAGGCGGAGAAATCGCTTGAACCCAGT 433
DB 1987 TGCATGCTGTAATCCAGCTACTTTGGAGGCTGAGGCGGAGAAATTTGCTTGAACCCGGG 2046
QY 434 AGGACAGGTTGAGTCCAGTCCGAGATGAAGATCACTGCACTCCAGCTGGGTGACAGG 493
DB 2047 A-GCAGAGGTTGAGTCCAGTCCGAGATCA-TGCCACTGCACTCCAGCTGGGTGACAGG 2104
QY 494 AAGACTCCCTCTCAGAAATAAAAA 522
DB 2105 GAGACTCCATTTCAAAAAAAGAACTACA 2133

RESULT 4

US-09-154-602-6
Sequence 6, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Frecci
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-154-602-6

Query March 28.4%; Score 284; DB 4; Length 2713;
Best Local Similarity 81.3%; Pred. No. 1.7e-55;
Matches 365; Conservative 0; Mismatches 81; Indels 3; Gaps 3;

QY 74 AATTAATGGAATAGGCTAGGCGGGTGGCTACGCGCTGTAATCCAGACACTTTAGAGG 133
DB 1688 AAAAAATCAAAATTTAGCGCGCGTGGTGGCTCACCTGTAATCCAGACTTTGGGAGG 1747
QY 134 TCGAAGAGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACGAGCTGGCCACACGGTGA 193
DB 1748 CTGAGCGAGGAGAAATCACTTGAGGTTCAGGAG-TTTGAGACCGAGCTGGCCACAGTGTGA 1806
QY 194 AACCCCATCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGTGGCTCACCTGTAATC 253
DB 1807 AACCTGTCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGAGGCGGGTGGCGCTGTAATC 1866
QY 254 CCAGACATTTGGGAGGCTGAGACGGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACGAGCTGGCCACACGGTGA 313
DB 1867 TCAGACATTTGGGAGGCGGAGGAGGTGGATCACTTGAGGTTCAGGAGTTTTCAGACACGAGCTGGCCACAGCC 1926
QY 314 TGGGCAACATGGTGAACACCGTCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGTGG 373
DB 1927 TGGCCAAACATGGTGAACACCGCTCTACTAAAAATAAAAAATTAAGTNGGGTGGCGTGG 1986
QY 374 CACAGCGCTGTAGTCCAGCTACTTTGGAGGCTGAGGCGGAGAAATCGCTTGAACCCAGT 433
DB 1987 TGCATGCTGTAATCCAGCTACTTTGGAGGCTGAGGCGGAGAAATTTGCTTGAACCCGGG 2046
QY 434 AGGACAGGTTGAGTCCAGTCCGAGATGAAGATCACTGCACTCCAGCTGGGTGACAGG 493
DB 2047 A-GCAGAGGTTGAGTCCAGTCCGAGATCA-TGCCACTGCACTCCAGCTGGGTGACAGG 2104
QY 494 AAGACTCCCTCTCAGAAATAAAAA 522
DB 2105 GAGACTCCATTTCAAAAAAAGAACTACA 2133

RESULT 5

US-09-318-448-5/c

; Sequence 5, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Johnson, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-5

Query Match 28.4%; Score 284; DB 3; Length 7720;
Best Local Similarity 84.9%; Pred. No. 2.1e-55;
Matches 376; Conservative 0; Mismatches 61; Indels 6; Gaps 5;

QY 87 AGCTAGGCGGGTGGCTCAAGCTGTAATCCAGACACTTTAGAGGTTCGAGAGGTGG 146
Db 6233 AGCTGGGTGAGTGGCTTACTTGTGTAATCCAGACACTTTGGAGGCCAAGCGAGGTGG 6174

QY 147 ATCACTTGAGTCAAGAGTTTGGAGCCAGCTGGCCACACAGGTGAAACCCCATCTCTA 206
Db 6173 ATCACTTGAGATCAAGAG-TTTGAGACCAGCTGGCCACACATGTGAAACCCCATCTCTA 6115

QY 207 CTAATAAATA-AAAAATTAGCTGGGTGGGTGGCTCACACCTGTGTAATCCAGACACTTTGG 265
Db 6114 CTAATAAATA-AAAAATTAGCTGGGTGGGTGGCTCACACCTGTGTAATCCAGACACTTTGG 6055

QY 266 GAGGCTGAGACGGGTGGATCACTGAAGTCAAGGTTCAAGCCAGCTGGCCACACATGG 325
Db 6054 GAGGCGAGGCGGTGGATCAC--GAGCTTGAAGATCAAGACCATCTCTGGCCACATGG 5997

QY 326 TGAACACAGCTCTCTACTAAAAATAC-AAAAATTAGCCAGGTGGTGGCACACGCTGT 384
Db 5996 TGAACACAGCTCTCTACTAAAAATACAAAAAATTAGCCGGGTGGTGGTGGCACCTGT 5937

QY 385 AGTCCACAGTCTTGGGAGGCTGAGCGGAGATCGCTTGAACCCAGTGGAGGATTT 444
Db 5936 AGTCCACAGTCTTGGGAGGCTGAGCGGAGGATGGTGAACCCGCGAGGTGGAGCTT 5877

QY 445 GCAGTGAGCCGAGATAAGATCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTC 504
Db 5876 GCAGTGAGCCGAGATCA-TGCCACTGCACTCCAGCTGGGGGACAGAGCAAGACTCCATC 5818

QY 505 TCAGAAAAATAAATAAATAAATA 527
Db 5817 TCAGAAAAATAAATAAATAAATA 5795

RESULT 6
US-09-801-861-3/c
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5332
; TYPE: DNA
; ORGANISM: Human

US-09-801-861-3

Query Match 28.0%; Score 279.6; DB 4; Length 5332;
Best Local Similarity 78.2%; Pred. No. 3e-54;
Matches 373; Conservative 0; Mismatches 100; Indels 4; Gaps 3;

QY 88 GGCTAGGCGGGTGGCTCAGCGCTGTAATCCAGACACTTTAGAGGTTCGAGAGGTGGGA 147
Db 25692 GGCCAGGCGGAGGACTCACAATGTGTAATCCAGAACTTTGAGAGGCCAAGCGAGGGA 25633

QY 148 TCACCTTGAGTCAAGAGTTTGGAGACCAAGCTGGCCAAACACGCTGAAACCCCATCTCTAC 207
Db 25632 TTGCTTGAGTCCAGGAG-TTCGAGACCAGCTGGGCAACATAGCAAGACCCCACTCTAT 25574

QY 208 TAAAAATAAATAAATTAGCTGGGTGGGTGGCTCACCTGTGTAATCCAGACACTTTGGGA 267
Db 25573 AAAAAACAAAAA--TAGGCCAGGCACAGTGGCTCATACCTGTGTAATCCAGACACTTTGGGA 25516

QY 268 GGCTGAGACGGGTGGATCACTGAAGTCAAGAGTTCAAGCCAGCTGGCCAAACATGGTG 327
Db 25515 GGCCAGGCGAGTGAATCACTCAGGTCAAGGTTCAGACCAAGCTGGCCACATGGTG 25456

QY 328 AAACACAGTCTCTACTAAAAATAAATAAATTAGCCAGGTGGTGGCACACGCTGTAGT 387
Db 25455 AAACCCCGTCTCTACTAAAAATAAATAAATTAGTCAAGTGGGTGGGTGGCTGTAGT 25396

QY 388 CCCAGCTACTTTGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTGGAGAGGTGCA 447
Db 25395 CCCAGCTACTTTGAGAGGCTGAGCGAGGAGGCTCCCTTTGAACCCAGGAAAGCGAGGTGCA 25336

QY 448 GTGAGCCGAGATAAGAGTCACTGCACTCAGCTGGGTGGTGGACAGAGCAAGCTCCCTCTCA 507
Db 25335 GTGAGCTGAG-TTTGGCCCACTGCACTCAGCTGGCGAGAGGAGACTCCCGTCTCA 25277

QY 508 GAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 564
Db 25276 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 25220

RESULT 7

US-08-257-963B-10
; Sequence 10, Application US/08257963B
; Patent No. 5840686
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, S.
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Tanikawa, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
; TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,963B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH

QY 387 TCCAGCTACTTGGGAGGCTGAGCGGAGAGATCGCTTGAACCCAGTAGGACAGGTTGC 446
|||||
Db 4055 TCCAGCCAGTACGAGGCTGAGCGAGGAGATCACTGGAATCCTGGAGTGGAGTTGC 4114
|||||
QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 506
|||||
Db 4115 AGTGAGCCGAGAT-GGTACCTCTGTACTCCAGCTGGGGACAGAGTGAAGTCCGCTCTC 4173
|||||
QY 507 AGAAATAAA 516
|||||
Db 4174 AAAAAAAAAA 4183
|||||

RESULT 9

PCT-US95-07201-10
; Sequence 10, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07201
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,841
; FILING DATE: 30-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7210 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; LIBRARY: DASH II
; FEATURE:
; NAME/KEY: JT6A
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: 7.0 kb Not 1-Not
; OTHER INFORMATION: fragment; derived from human placental

; OTHER INFORMATION: genomic DNA; also referred to as JT106
PCT-US95-07201-10

Query Match 27.8%; Score 277.8; DB 5; Length 7210;
Best Local Similarity 82.3%; Pred. No. 5.2e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GGCTAGGCGGGTGGCTCAAGCTGTATCCCGACACTTTAGAGGTGCAAGAGGGTGA 147
|||||
Db 3756 GGCGGGGACGGTGGCTCAAGCTGTATCCCGACACTTTGGAGGCCGAGCAGCAGA 3815
|||||
QY 148 TCACCTGAGGTGAGGAGTTTGGACACAGCCTGGCCACACGGTGAACCCCATCTCTAC 207
|||||
Db 3816 TCACCTGAGGTGAGGAG-TTCGAGACAGCCTGGCTTAACAGATGAACCCGCTCTCTAC 3874
|||||
QY 208 TAAAAATA-AAAAAATTAGCTGGGTGGGTGCTCACACCTGTAAATCCCGACACTTTGGG 266
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Db 3875 TAAAAATA-AAAAAATTAGCTGGGTGGGTGCTCTGTGCTGTAAATCCCGACACTTTGGG 3934
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QY 267 AGGCTGAGACGGGTGGATCACCTGAAAGTCAGGAGTTCAAGGCCAGCCTGGGCAACATGGT 326
|||||
Db 3935 AGGCAGAGGTGGGACATCACTTGAGGTTCAGGAGTTTGACACAGCCTAGCCACATGGT 3994
|||||
QY 327 GAAACACAGCTCTCTACTATAAAATAAAAAATTAGCCAGGTGTGGTGACACAGCCTGTAG 386
|||||
Db 3995 GAAACCCCATCTCTACTATAAACTACAAAAATTAGCCGAGGTGTGGTGACACGCTGTAA 4054
|||||
QY 387 TCCGAGCTACTTGGGAGGTGAGCGGAGAGATCGCTTGAACCCAGTAGGACAGGTTGC 446
|||||
Db 4055 TCCGAGCAGTTCAGGAGGCTGAGCGAGGAGATCACTGGAATCCTGGAGGTGGAGTGGC 4114
|||||
QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 506
|||||
Db 4115 AGTGAGCCGAGAT-GGTACCTCTGTACTCCAGCTGGGGACAGAGTGAAGTCCGCTCTC 4173
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QY 507 AGAAATAAA 516
|||||
Db 4174 AAAAAAAAAA 4183
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RESULT 10

US-08-520-373D-4
; Sequence 4, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 14581
; TYPE: DNA HUMAN
; ORGANISM:
; FEATURE:
; OTHER INFORMATION: mRNA: 6683; EXON: 6683; EXON: 6683-6790; EXON 11584-11675;
; OTHER INFORMATION: INTRON: 6791-11583; INTRON:
; OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580

US-08-520-373D-4

Query Match 27.8%; Score 277.8; DB 4; Length 14581;
Best Local Similarity 82.3%; Pred. No. 5.9e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GGTAGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTAGAGGTCGAAGAGGTGGA 147
Db |||||
3755 GCGCGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTAGAGGTCGAAGAGGTGGA 147
Db |||||

QY 148 TCACITTAGGTCAGGAGTTTGTAGACCAAGCTGCGCAACACAGGTGAAACCCCATCTCTAC 207
Db |||||

QY 3815 TCACITTAGGTCAGGAG-TTCGAGACCAAGCTGCTTAACACATGAACCCCTCTCTAC 3873
Db |||||

QY 208 TAAATA-AAAAATTAGCTNGGCTGCGTCTACACCTGTATCCAGCACTTTGGG 266
Db |||||

QY 3874 TAAATAACAAAAATTAGCTGGCGACGGTGGCTCGTCTGTATCCAGCACTTTGGG 3933
Db |||||

QY 267 AGGCTGAGCGGTGATCACCCTGAAGTCAGGAGTTCAAGGCCAGCTGGGCAACATGGT 326
Db |||||

QY 3934 AGGAGAGGTGGCGAGTCACTTGAGGTCAGGAGTTTGAGACCAAGCTAGCCAAACATGGT 3993
Db |||||

QY 327 GAAACCAAGCTCTCTACTTAAATAACAAAAATTAGCCAGGTGCTGCGCAACAGCTGTAG 386
Db |||||

QY 3994 GAAACCAAGCTCTCTACTTAAATAACAAAAATTAGCCAGGTGCTGCGCAACAGCTGTAG 4053
Db |||||

QY 387 TCCAGCTACTTTGGGAGGTGAGCGGAGAAATCGCTTGAACCCAGTAGGAGGTTGC 446
Db |||||

QY 4054 TCCAGCGAGTCAGGAGGCTGAGGCGAGGAGATCACTGGAATCTCTGGAGGTGGGTCGC 4113
Db |||||

QY 447 AGTGAGCGAGATAAGAGTCACTGCACTCCAGCGCTGGGTGACAGACAGACTCCCTCTC 506
Db |||||

QY 4114 AGTGAGCGAGAT-GGTACTCTGTACTCCAGCTGGGGGACAGAGTGAGACTCGGTCTC 4172
Db |||||

QY 507 AGAAAAATAA 516
Db |||||

QY 4173 AAAAAAATAA 4182
Db |||||

RESULT 11

US-08-367-841A-43
; Sequence 43, Application US/08367841A
; Patent No. 6319687
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Rodriguez,
; APPLICANT: Ignacio R.; Mazurk, Krzysztof;
; APPLICANT: Tombran-Tink, Joyce
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,841A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: PI-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
; OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-367-841A-43

Query Match 27.8%; Score 277.8; DB 4; Length 22481;
Best Local Similarity 82.3%; Pred. No. 6.4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GGTAGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTAGAGGTCGAAGAGGTGGA 147
Db |||||

QY 3748 GCGCGGCGCGGTGCTCAGCGCTGTATCCAGCACTTTAGAGGTCGAAGAGGTGGA 147
Db |||||

QY 148 TCACITTAGGTCAGGAGTTTGTAGACCAAGCTGCGCAACACAGGTGAAACCCCATCTCTAC 207
Db |||||

QY 3808 TCACITTAGGTCAGGAG-TTCGAGACCAAGCTGCTTAACACATGAACCCCTCTCTAC 3866
Db |||||

QY 208 TAAATA-AAAAATTAGCTNGGCTGCGTCTACACCTGTATCCAGCACTTTGGG 266
Db |||||

QY 3867 TAAATAACAAAAATTAGCTGGCGACGCTCGTCTGTATCCAGCACTTTGGG 3926
Db |||||

QY 267 AGGCTGAGCGGTGATCACTGAGTCAGGAGTTCAAGGCCAGCTGGGCAACATGGT 326
Db |||||

QY 3927 AGGAGAGGTGGCGAGATCACTTGAGGTCAGGAGTTGAGACCAAGCTAGCCAAACATGGT 3986
Db |||||

QY 327 GAAACCAAGCTCTCTACTTAAATAACAAAAATTAGCCAGGTGCTGCGCAACAGCTGTAG 386
Db |||||

QY 3987 GAAACCAAGCTCTCTACTTAAATAACAAAAATTAGCCAGGTGCTGCGCAACAGCTGTAG 4046
Db |||||

QY 387 TCCAGCTACTTTGGGAGGTGAGCGGAGAAATCGCTTGAACCCAGTAGGAGGTTGC 446
Db |||||

QY 4047 TCCAGCGAGTCAGGAGGCTGAGGCGAGGAGATCACTGGAATCTCTGGAGGTGGAGTGGC 4106
Db |||||

QY 447 AGTGAGCGAGATAAGAGTCACTGCACTCCAGCGCTGGGTGACAGACAGACTCCCTCTC 506
Db |||||

QY 4107 AGTGAGCGAGAT-GGTACTCTGTACTCCAGCTGGGGGACAGAGTGAGACTCGGTCTC 4165
Db |||||

QY 507 AGAAAAATAA 516
Db |||||

QY 4166 AAAAAAATAA 4175
Db |||||

RESULT 12

PCT-US95-07201-43
; Sequence 43, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Paniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: PL-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
PCT-US95-07201-43

Query Match 27.8%; Score 277.8; DB 5; Length 22481;
Best Local Similarity 82.3%; Pred. No. 6.4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GGCTAGGCGCGGTGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTCGAGAGGGTGA 147
Db 3748 GGCGGGACGGTGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTCGAGAGGGTGA 147

QY 148 TCACCTGAGGTCAGGAGTTTGGAGACCGCTGGCCAAACACCGGTGAACCCCATCTCTAC 207
Db 3808 TCACCTGAGGTCAGGAG-TTCGAGACCGCTGGCTTAACACGATGAACCCCGTCTCTAC 3866

QY 208 TAAAAATA-AAAAAATTAGCTNGGTCGGTGGCTCAACCTGTAAATCCAGCACTTTGGG 266
Db 3867 TAAAAATA-AAAAAATTAGCTNGGTCGGTGGCTCAACCTGTAAATCCAGCACTTTGGG 3926

QY 267 AGGCTGAGACCGGTGGATCACTGAAAGTCAGGAGTTCAAGCCAGCTGGGCAACATGT 326
Db 3927 AGGCGAGGTGGGCGAGTCACTTGAGGTCAGAGTTTGAGACCGCTTAGCAACATGT 3986

QY 327 GAAACCACTCTCTACTAAATAATACAAAAATTAGCCAGGTGTGGTGACACCGCTGTAG 386
Db 3987 GAAACCCCATCTCTACTAAATAATACAAAAATTAGCCAGGTGTGGTGACACCGCTGTAG 4046

QY 387 TCCAGCTACTTTGGGAGGCTGAGCGGAGAGTCCCTTGAACCCAGTAGGAGGTTGC 446
Db 4047 TCCAGCGAGTCAGGAGGCTGAGCGGAGAGTCACTTGAATCCTGGAGGTGGAGGTGC 4106

QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 506
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QY 507 AGAATAAA 516
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Db 4107 AGTGAGCCGAGAT-GGTACTCTGTACTCCAGCTGGGTGACAGAGTGAAGTCCCTCTC 4165

QY 507 AGAATAAA 516
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Db 4166 AAAAAAAAAA 4175
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RESULT 13
US-09-875-223-2
; Sequence 2, Application US/09875223
; Patent No. 6391850
; GENERAL INFORMATION:
; APPLICANT: No. 6391850thwestern University
; APPLICANT: No. 63918501 Bouck
; APPLICANT: David Dawson
; APPLICANT: Paul Gillis
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
; FILE REFERENCE: 0290-23U3
; CURRENT APPLICATION NUMBER: US/09/875,223
; PRIORITY FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 22484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1...22484
; OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-223-2

Query Match 27.8%; Score 277.8; DB 4; Length 22484;
Best Local Similarity 82.3%; Pred. No. 6.4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GGCTAGGCGCGGTGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTCGAGAGGGTGA 147
Db 3748 GGCGGGACCGTGGCTCAGCGCTGTAATCCCGACACTTTGGGAGCGCGAGGCGAGA 3807

QY 148 TCACCTGAGGTCAGGAGTTTGGAGACCGCTGGCCAAACACCGGTGAACCCCATCTCTAC 207
Db 3808 TCACCTGAGGTCAGGAG-TTCGAGACCGCTGGCTTAACACGATGAACCCCGTCTCTAC 3866

QY 208 TAAAAATA-AAAAAATTAGCTNGGTCGGTGGCTCAACCTGTAAATCCAGCACTTTGGG 266
Db 3867 TAAAAATA-AAAAAATTAGCTNGGTCGGTGGCTCAACCTGTAAATCCAGCACTTTGGG 3926

QY 267 AGGCTGAGACCGGTGGATCACTGAAAGTCAGGAGTTCAAGCCAGCTGGGCAACATGT 326
Db 3927 AGGCGAGGTGGGCGAGTCACTTGAGGTCAGAGTTTGAGACCGCTTAGCAACATGT 3986

QY 327 GAAACCACTCTCTACTAAATAATACAAAAATTAGCCAGGTGTGGTGACACCGCTGTAG 386
Db 3987 GAAACCCCATCTCTACTAAATAATACAAAAATTAGCCAGGTGTGGTGACACCGCTGTAG 4046

QY 387 TCCAGCTACTTTGGGAGGCTGAGCGGAGAGTCCCTTGAACCCAGTAGGAGGTTGC 446
Db 4047 TCCAGCGAGTCAGGAGGCTGAGCGGAGAGTCACTTGAATCCTGGAGGTGGAGGTGC 4106

QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 506
Db 4107 AGTGAGCCGAGAT-GGTACTCTGTACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTC 4165

QY 507 AGAATAAA 516
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Job time : 94 secs

RESULT 15
 US-03-729-995-3
 ; Sequence 3, Application US/09729995
 ; Patent No. 6426206
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 15:31:06 ; Search time 351 Seconds
(without alignments)
10383.352 Million cell updates/sec

Title: US-09-784-423-32

Perfect score: 1000

Sequence: 1 GGTGTACCTTATCTCTCT.....CAGATGATGACCGCGTGC 1000

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	320.2	32.0	7017	10	US-09-764-877-3773
3	320.2	32.0	7017	12	US-10-242-515-3773
4	320.2	32.0	20522	10	US-09-764-877-3774
5	320.2	32.0	20522	12	US-10-242-515-3774
6	311.8	31.2	17588	12	US-10-292-798-1277
7	311.8	31.2	17588	13	US-10-017-161-1603
8	307.2	30.7	31703	12	US-10-085-117-172
9	307.2	30.7	53106	13	US-10-034-650-10
10	307	30.7	174424	10	US-09-967-768A-314
11	307	30.7	174424	13	US-09-960-706-969
12	304.2	30.4	113000	13	US-10-376-566-16
13	303.4	30.3	27087	12	US-10-292-798-1279
14	303.4	30.3	27087	13	US-10-017-161-1605
15	301.4	30.1	174424	10	US-09-967-768A-314

Sequence 969, Appl
Sequence 3, Appl
Sequence 30, Appl
Sequence 11, Appl
Sequence 1349, Ap
Sequence 7789, Ap
Sequence 7788, Ap
Sequence 3, Appl
Sequence 3, Appl
Sequence 3428, Ap
Sequence 22, Appl
Sequence 22, Appl
Sequence 123503,
Sequence 123503,
Sequence 123503,
Sequence 5477, Ap
Sequence 10204, A
Sequence 1003, Ap
Sequence 1, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 34, Appl
Sequence 1, Appl
Sequence 191490,
Sequence 191491,
Sequence 191490,
Sequence 191491,
Sequence 24794, A
Sequence 24794, A
Sequence 363, App

ALIGNMENTS

RESULT 1

US-09-784-423-32

/ Sequence 32, Application US/097844423

/ Patent No. US20020012924A1

/ GENERAL INFORMATION:

/ APPLICANT: Schumm, James W.

/ Bacher, Jeffery W.

/ TITLE OF INVENTION: MATERIALS AND METHODS FOR

/ IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

/ REPEAT DNA MARKERS

/ NUMBER OF SEQUENCES: 147

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Promega Corporation

/ STREET: 2800 Woods Hollow Road

/ CITY: Madison

/ STATE: Wisconsin

/ COUNTRY: U.S.A.

/ ZIP: 53711-5399

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB

/ COMPUTER: IBM compatible PC

/ OPERATING SYSTEM: Windows 95

/ SOFTWARE: Word 97 (DOS text format)

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/784,423

/ FILING DATE: 15-Feb-2001

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 09/018,584

/ FILING DATE: 04-Feb-1998

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Grady J. Frenchick

/ REGISTRATION NUMBER: 29,018

/ REFERENCE/DOCKET NUMBER: 16026.9180

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (608) 257-3501

/ TELEFAX: (608) 257-2275

/ INFORMATION FOR SEQ ID NO: 32

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SEQUENCE CHARACTERISTICS:
LENGTH: 1000 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
IMMEDIATE SOURCE:
CLONE: S132
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 22
SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      99.9%; Score 999; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 5e-241;
Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACCTTATCTCTCTGAACTCAGTTTCTCTCATCGTAAATGAAAGCTGTAG 60
DB 1 GGTGTGACCTTATCTCTCTGAACTCAGTTTCTCTCATCGTAAATGAAAGCTGTAG 60
QY 61 ATTGTTGTAATAAATAAATGAATAGGCTAGGCGGGTGGCTCAGCCCTGTAATCCCA 120
DB 61 ATTGTTGTAATAAATAAATGAATAGGCTAGGCGGGTGGCTCAGCCCTGTAATCCCA 120
QY 121 GCATTTAGAGGTGCGAAGGGTGTATCACTTGAAGTCAGGAGTTTGTAGACAGCCTG 180
DB 121 GCATTTAGAGGTGCGAAGGGTGTATCACTTGAAGTCAGGAGTTTGTAGACAGCCTG 180
QY 181 GCCAACACGGTGAACCCCATCTCTACTATAAATAAATAAATAGCTGGTGGCT 240
DB 181 GCCAACACGGTGAACCCCATCTCTACTATAAATAAATAAATAGCTGGTGGCT 240
QY 241 CACACTGTATPCCAGCACTTTGGGAGGCTGAGACGGGTGATCACTCAAGTCAGGAG 300
DB 241 CACACTGTATPCCAGCACTTTGGGAGGCTGAGACGGGTGATCACTCAAGTCAGGAG 300
QY 301 TTCAGGCGCCCTGGGCAACATGTGTAACACGCTCTCTACTATAAATAAATAAATAG 360
DB 301 TTCAGGCGCCCTGGGCAACATGTGTAACACGCTCTCTACTATAAATAAATAAATAG 360
QY 361 CCAGGTGTGGTGGCAGACCGCTGTAGTCCAGCTTCTGGGAGGCTGAGCGGAGATC 420
DB 361 CCAGGTGTGGTGGCAGACCGCTGTAGTCCAGCTTCTGGGAGGCTGAGCGGAGATC 420
QY 421 GCTTGAACCCAGTAGGACAGGTTGCACTGAGCGGAGATGAGTCACTGCACTCCAGCC 480
DB 421 GCTTGAACCCAGTAGGACAGGTTGCACTGAGCGGAGATGAGTCACTGCACTCCAGCC 480
QY 481 TGGGTGACAGAGCAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
DB 481 TGGGTGACAGAGCAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
QY 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
DB 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
QY 601 AGTATAGCTATCAATATCCCAACCCCTACCCTGCTGCTGAAATTTAGTTTCTTTTGT 660
DB 601 AGTATAGCTATCAATATCCCAACCCCTACCCTGCTGCTGAAATTTAGTTTCTTTTGT 660
QY 661 ACCCCCAATTAGACTTAAAGCAGAAATCTCACCGTACTCTCTGTAATTTCTGTTTCT 720
DB 661 ACCCCCAATTAGACTTAAAGCAGAAATCTCACCGTACTCTCTGTAATTTCTGTTTCT 720
QY 721 GGCACATAGTTGGGTCTCAGTGAACATGTTGAGTGAATGAGCAATGCAAGGAATCTCC 780
DB 721 GGCACATAGTTGGGTCTCAGTGAACATGTTGAGTGAATGAGCAATGCAAGGAATCTCC 780
QY 781 AGGCCATCTGGGAGCCCTCCAGCGGGTGTAGTTCGGGAAATCTCATAGTCTCTCTCAAT 840
DB 781 AGGCCATCTGGGAGCCCTCCAGCGGGTGTAGTTCGGGAAATCTCATAGTCTCTCTCAAT 840
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QY 841 GGGCCACTGAAGGTAGAGAGTTCTGGTCCCACTCTCGGACCCCCATCTCTGACTCAC 900
DB 841 GGGCCACTGAAGGTAGAGAGTTCTGGTCCCACTCTCGGACCCCCATCTCTGACTCAC 900
QY 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
DB 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
QY 961 CAGGACTGCAAGGAGGCCAGCAGAAATGATGACCGCGGTGC 1000
DB 961 CAGGACTGCAAGGAGGCCAGCAGAAATGATGACCGCGGTGC 1000
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RESULT 2

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US-09-764-877-3773/c
; Sequence 3773, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3773
; LENGTH: 7017
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3773
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Query Match      32.0%; Score 320.2; DB 10; Length 7017;
Best Local Similarity 84.6%; Pred. No. 6e-70;
Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;
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QY 86 TAGGCTAGCGCGGTGGCTCAGCCCTGTAAATCCAGCACTTTAGAGGTGAGAGGGTG 145
DB 4509 TGGGCCAGACGGCGTGGCTCACACCTGTATCCAGCACTTTGGAAGCGCGGGTG 4450
QY 146 GATCACTTCAAGTCAGGAGTTTGTAGACACAGCCTGGCCAAACAGCGTGAACCCCATCTCT 205
DB 4449 GATCACTTCAAGTCAGGAGTTTGTAGACACAGCCTGGCCAAACAGCGTGAACCCCATCTCT 4391
QY 206 ACTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 265
DB 4390 ACTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4331
QY 266 GAGGCTGAGACGGGTGGATCACTCAAGTCAGGAGTTCAAGCCAGCTGGGCAACATGG 325
DB 4330 GAGGCTGAGACGGGTGGATCACTCAAGTCAGGAGTTCAAGCCAGCTGGGCAACATGG 4273
QY 326 TGAACCAAGCTCTCTACTAAAAATACAAAAATTTAGCAGGTGTGGTGGCAACGCTGTA 385
DB 4272 TGAACCAAGCTCTCTACTAAAAATACAAAAATTTAGCAGGTGTGGTGGCAACGCTGTA 4213
QY 386 GTCCAGCTACTTGGGAGGCTGAGCGGAGAAATCCTTGAACCCAGTGTAGGAGGTTG 445
DB 4212 GTCCAGCTACTTGGGAGGCTGAGCGGAGAAATCCTTGAACCCAGTGTAGGAGGTTG 4153
QY 446 CAGTGAAGCGGAGATGAGTCACTGCACTCCAGCTGGGTGGTGGCAACGAGTCCCTCT 505
DB 4152 CAGTGAAGCGGAGATGAGTCACTGCACTCCAGCTGGGTGGTGGCAACGAGTCCCTCT 4094
QY 506 CAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
DB 4093 CA-AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4035
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RESULT 3

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US-10-242-515-3773/c
; Sequence 3773, Application US/10242515
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RESULT 4
US-09-764-877-3774/c
; Sequence 3774, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3774
; LENGTH: 20522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3774

Query Match          32.0%; Score 320.2; DB 10; Length 20522;
Best Local Similarity 84.6%; Pred. No. 9,8e-70;
Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;

QY      86  TAGGCTAGGCGCGGTGGCTCACGCCCTGTGAATCCAGACATTTTAGAGGTGCGAAGAGGGTG 145
Db      10327 TGGGCCAGACGGCGGTGGCTCACACTGTATTCCAGCATTTTGAAGCGCGAGGCGGGTG 10268

QY      146  GATCACTTGAAGTTCAGGAGTTTGTAGACCCAGCTGGCCCAACACGGTGAACCCCATCTCT 205
Db      10267 GATCACTTGAAGNCAAGAG-TTCGAGACAGCTGGCCCAACATGGTGAACCTGCTCTCT 10209

QY      206  ACTAAATAATAAAATAGTNGGTGGCGGTGCTCACACCTGTGAATCCAGCATTTGG 265
Db      10208 ACTAAATAATCAAAATTTGACTGGCGGAGTGGCTCACACTGTGATCCCACTATTTGG 10149

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QY	266	GAGGCTCAGACGGGTGAGTCACTCACTCAAGTTCAGGAGTTACGCCACGCTGGGCACACATGG	325
Db	10148	GAGGCCAAGCGCGGCGAGATCA--TGAGGTCAGAAGATGGAGACCATCTCTGGCTAACATGG	10091
QY	326	TGAACACCACGTCCTCTACTAAAAATCAAAAATTAGCCAGGTGTGGTGGCAGACCGCTGTA	385
Db	10090	TGAAACCCGTCCTCTACTAAAAATCAAAAATTAGCCAGGATGGTGGCAGACCGCTGCA	10031
QY	386	GTCCGAGCTACTTGGGAGGCTTGAGCGGAAGAAATCGCTTGAACCCAGTAGGACAGCGTTG	445
Db	10030	GTCCGAGCTACTCAGGAGGCTGAGCAGGAGATAGCCTGAAACCCAGGAGGCGGAGTTG	9971
QY	446	CAGTGAAGCCGAGATAAGTGCATCGACTCCAGCTCGGGTCAGAGCAGAAGTCTCCCTCT	505
Db	9970	CAGTGAAGCCGAGATCA--CGACACTCGCTCCAGCTGGGCAACAGAGCGAAGTCCGCTCT	9912
QY	506	CAGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATCTTAAAA	565
Db	9911	CA-AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA	9853

RESULT 5

US-10-242-515-3774/c

; Sequence 3774, Application US/10242515

; Publication No. US20040009488A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC005C1

; CURRENT APPLICATION NUMBER: US/10/242,515

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 09/764,877

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: 60/214,886


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; PRIOR FILING DATE: 2000-05-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3774
; LENGTH: 20522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3774

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	Query Match	32.0%;	Score	320.2;	DB 12;	Length	20522;	
	Best Local Similarity	84.6%;	Pred.	No. 9.8e-70;	Mismatches	69;	Gaps	5;
	Matches	406;	Conservative	0;	Mismatches	69;	Indels	5;
QY	86	TAGCTGACGGCGGTGCCTCAGCCCTGTAAATCCCAGCACTTTTAGAAGTTCGAAGAGGGTG	145					
Db	10327	TGGGCCAGACGGGTGGCTCACACTTGTATTCCAGCACTTTTGGAGAAGCCGAGCGGGTG	10268					
QY	146	GATCACTTCAGAGTCAGGAGTTTTGAGACCAGCTTGGCCAACGGGTGAACCCCATCTCT	205					
Db	10267	GATCACTTGAAGACAAGAG--TTCAGAACCAAGCTTGGCCCAACATGTGTGAACCTCGTCTCT	10209					
QY	206	ACTAAAAATAAAAANTTAGCTNGSGTGGCTGCACACTGTAAATCCCCAGCACTTTGG	265					
Db	10208	ACTAAAAATACAAAAATTTGACTGGCGCAGTGGCTCACACTGTTACCCAGCACTTTGG	10149					
QY	266	GAGSCTGACAGCGGTGGATCACTTGAAGTTCAGGAGTTTCAAGGCCAGCTGGGCNAACATGG	325					
Db	10148	GAGGCCAAGCGCGGCAGATCA--TGAGSTCAAGAGATGGAGACATCTCTGGCTTAACATGG	10091					
QY	326	TGAAAACACAGCTCTCTACTAAAAATAACAAAAATAGCCAGGTGTGTGGCCACAGCCCTGTA	385					
Db	10090	TGAAACCCCGTCTCTACTAAAAATAACAAAATTTAGCCAGGCATGGTGGCAACAGCCTGCA	10031					
QY	386	GTCCGAGCTACTTGGGAGGCTGAGCGCGAAGAAATCGTTGAACCCAGTAGGCAGAGGTG	445					
Db	10030	GTCCGAGCTACTCAGGAGGCTGAGCGAGGAGAATAGCTTGAACCCAGAGCGCGGAGGTG	9971					
QY	446	CAGTGAAGCCGATAGAGTCACTGCACTCCAGCTCGGTGTGACAGCAAGACTCCCTCT	505					
Db	9970	CAGTGAAGCCGAGATCA-CGACACTGCACTCCAGCGCTGGGCCAACAGAGCGAGAACTCCGTCT	9912					
QY	506	CAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	565					
Db	9911	CA-AATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	9853					

RESULT 6
US-10-292-798-1277/c
; Sequence 1277, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIORITY FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161

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: PRIOR FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: JP 2001-246789
: PRIOR FILING DATE: 2001-06-18
: NUMBER OF SEQ ID NOS: 2070
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1277
: LENGTH: 17588
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: LOCATION: source
: FEATURE:
: LOCATION: (1)..(17588)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (201)..(386)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (660)..(873)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (2837)..(3270)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (3360)..(3460)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (12023)..(12329)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (17307)..(17388)
: FEATURE:
: NAME/KEY: modified base
: LOCATION: (6225)..(6324)
: OTHER INFORMATION: a, t, c, g, unknown or other
: FEATURE:
: NAME/KEY: modified base
: LOCATION: (12380)..(12479)
: OTHER INFORMATION: a, t, c, g, unknown or other
: US-10-292-798-1277

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Query Match	31.2%	Score 311.8	DB 12	Length 17588
Best local Similarity	80.6%	Pred. No. 1.2e-67		
Matches 400	Conservative 0	Mismatches 93	Indels 3	Gaps 3
QY	61	ATTGTTGTAAAAAAATTAAATGGAATAGAGCTAGAGCGCGGTGCTCAGCGCTGTATATCCCA	120	
Db	15288	ATTTCATTAATAAACTGCTCTGTGAGCGCGGGGAGTGGTTCACATCTCTGTAAATCCCA	15229	
QY	121	GCACCTTTGAAAGTGCAGAGAGGTGGATCACTTTGAGGTCAGAGCTTTTGAGACACAGCGCTG	180	
Db	15228	GCACCTTTGCGAGGCCAAAGTGGGTGATCACTTTGAGGCCAGGAG-TTTTGAGACACAGCGCTG	15170	
QY	181	GCACACAGGTGAAACCCCATCTCTACTATAAAATAAAAAATAAAATTTAGCTNGGGTCGGTGCT	240	
Db	15169	GCACACATGCGAAACTCTGTCTCTACTAAAAATAACAATAATTTGGTCGGGCGCAGTAGCT	15110	
QY	241	CACACCTGTATATCCAGACACTTTTGGAGGCTTGAGACGGGTGGATCACTGAAATGACAGAG	300	
Db	15109	CACACCTGTATATCCCAACACTTTTGGAGGCGGAGGCGGGATTCCTTGAGGTCAGAG	15050	
QY	301	TTACAGCGCAGCTGGGCACATGCTGAAACCAAGTCTCTACTTAAAAATAAAAAATTAG	360	
Db	15049	TTACAGACACAGTCTGGCCAAATATGGTGAACCCCATCTCTACTAAAAATAAAAAATTAG	14990	
QY	361	CCAGGTGTGTTGSCACACGCGCTGTAGTCCACAGCTACTCTGGGAGGCTGAGGCGGAGGAATC	420	
Db	14989	CGGGGTGTGTCGACAGCGCTGTAAATCCAGCTACATGGAGGCTTGAGGCACAGAGAAATC	14930	
QY	421	GCTTTGAACCCATAGGCAGAGGTTGCAGTGAAGCCGAGATAAGATCACTGCACTCCAGCC	480	
Db	14929	ACTTGAACCCAGAGGAGGAGGTTGCAGTGAAGCCAGAT-CTGCGCACTGCACTCCAGCC	14871	

QY 481 TGGGTGACAGCAGCAGCTCCCTCTCAGAAAATAAATAAATAAATAAATAAATAAATAA 540
Db 14870 T-GGCAACAGAGCAGCAGCTCTGTCTCAAAAATAAATAAATAAATAAATAAATAA 14812
QY 541 AATAAAATAAATAA 556
Db 14811 AATAAATAAATAA 14796

RESULT 7

US-10-017-161-1603/c
; Sequence 1603, Application US/10017161
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SOWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1603
; LENGTH: 17588

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: source

LOCATION: (1)..(17588)

FEATURE:

NAME/KEY: CDS

LOCATION: (201)..(386)

FEATURE:

NAME/KEY: CDS

LOCATION: (660)..(873)

FEATURE:

NAME/KEY: CDS

LOCATION: (2637)..(3270)

FEATURE:

NAME/KEY: CDS

LOCATION: (3360)..(3460)

FEATURE:

NAME/KEY: CDS

LOCATION: (12023)..(12329)

FEATURE:

NAME/KEY: CDS

LOCATION: (17307)..(17388)

FEATURE:

NAME/KEY: modified base

LOCATION: (6225)..(6324)

FEATURE:

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified base

LOCATION: (12380)..(12479)

FEATURE:

OTHER INFORMATION: a, t, c, g, unknown or other

US-10-017-161-1603

Query Match 31.2%; Score 311.8; DB 13; Length 17588;
Best Local Similarity 80.6%; Pred. No. 1.2e-67;
Matches 400; Conservative 0; Mismatches 93; Indels 3; Gaps 3;

QY 61 ATTGTTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 120
Db 15288 ATTGATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15229

QY 121 GCATTTAGAGGTCGAAGAGGCTGGATCACTTAGGTGAGGAGTTTGGAGCCAGCCTG 180
Db 15228 GCATTTCGGAGGCAAAAGTGGTGGATCACTTAGGCCAGGAG-TTTGAGACCAGCTG 15170

QY 181 GCCACACGCTGAACCCCATCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAA 240
Db 15169 GCCACATGGCAAACTCTGTCTCTACTAAAAATAAATAAATAAATAAATAAATAA 15110
QY 241 CACACCTGTAATCCAGCAGCTTTGGGAGGCTGAGACGGGTGATCACCTCAAGTCAGGAG 300
Db 15109 CACACCTGTAATCCACACCTTTGGAGGCGGCGGCGGATTAATCTGAGTCAGGAG 15050
QY 301 TTCAAGGCCAGCTGGGCAACATGGTGAACACGCTCTCTACTAAAAATAAATAAATAA 360
Db 15049 TTCAAGACCACTGTGGCCAATATGTCGAACCCCATCTCTACTAAAAATAAATAA 14990
QY 361 CCAGGTGTGGTGGCAGACGCTGTAGTCCAGCTACTTTGGGAGGCTGAGCGGAAGATC 420
Db 14989 CCGGGTGTGGTGGCAGACGCTGTAGTCCAGCTACTTTGGGAGGCTGAGCGGAAGATC 14930
QY 421 GCTGAACCCAGTAGGACAGAGGTTGCAGTGCAGCCGAGATAAGAGTCACTCTCATCCAGCC 480
Db 14929 ACTTGAACCCAGGAGGAGGAGGTTGCAGTGCAGCCAGAT-CTCCGCACTGCCTCAGCC 14871
QY 481 TGGGTGACAGCAGCAGCTCCCTCTCAGAAAATAAATAAATAAATAAATAAATAAATAA 540
Db 14870 T-GGCAACAGAGCAGCAGCTCTGTCTCAAAAATAAATAAATAAATAAATAAATAA 14812
QY 541 AATAAAATAAATAA 556
Db 14811 AATAAATAAATAA 14796

RESULT 8

US-10-085-117-172/c
; Sequence 172, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 31703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(31703)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-172

Query Match 30.7%; Score 307.2; DB 12; Length 31703;
Best Local Similarity 80.6%; Pred. No. 2.2e-66;
Matches 407; Conservative 0; Mismatches 94; Indels 4; Gaps 4;

QY 47 TGAAGAAGCTGTAGATTGTTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 106
Db 3753 TGACAGAGTGAGACCCCTTTAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 3694
QY 107 CGCTGTAAATCCCGACCTTTAGAGGTGCGAAGGCTGGATCACTTGGAGTCAGAGTT 166
Db 3693 CACTGTAAATCCCGACCTTTAGAGGCGGAGGCTGGTGGAT-ACCTGAGCCAGGAG-T 3636
QY 167 TTGAGACCAGCTGGCCCAACAACCGTGAACCCCATCTCTACTAAAAATAAATAAATAA 225
Db 3635 TGGAGACCAGCTGGCAACAACGTGGAACCCCATCTTACTAAAAATAAATAAATAAATAA 3576
QY 226 TNGGGTGGCGGTGGCTACACCTGTAATCCAGCAGCTTTGGGAGGCTGAGACGGGTGGATC 285
Db 3575 CCAGGCAAGTGGCTCACCTGTAATCCAGCAGCTTTGGGAAGCTGTGGCGGCGAGATC 3516

QY 286 ACCTGAAGTCAGGAGTTCAGAGCCAGCCTGGGCAACATGCTGAACACACGCTCTACTAA 345
Db |||||
QY 3515 ACCTGAGGTCAGGAGTTCGAGACACAGCCTGACCAACATGCTGAACCCGCTCTACTAA 3456
Db |||||
QY 346 AATATCAAAAATAGCAGAGTGTGGGCAACGCGCTGTAGTCCAGCTACTTTGGGAGGC 405
Db |||||
QY 3455 AATATCAAAAATAGCAGAGTGTGGGCAACGCGCTGTAGTCCAGCTACTCAGGAGGC 3396
Db |||||
QY 406 TGAGGCGGAAGAATCGCTTGAACCCAGTAGGACAGAGTTCAGCTAGCCGAGATAGAGT 465
Db |||||
QY 3395 TGAGCAGGATATCGCTTGAACCCAGGAGCAGAGTTCAGCTAGCCAGATCA-CGC 3337
Db |||||
QY 466 CACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCCTCTCAGAAAAATAAATAAATA 525
Db |||||
QY 3336 CACTGCACTCCAGCCTGGGTGACAGAGTTCAGCTACTCTCAAAAAAATAAATAAATA 3277
Db |||||
QY 526 AATAAATAAATAAATAAATAAATAA 550
Db |||||
QY 3276 AAAAAAGAAAAAGAAAAACAAA 3252
Db |||||

RESULT 9
US-10-034-650-10
; Sequence 10, Application US/10034650
; Publication No. US20030216558A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000128
; CURRENT APPLICATION NUMBER: US/10/034,650
; PRIOR FILING DATE: 2002-07-23
; PRIOR FILING DATE: 1999-12-29
; PRIOR FILING DATE: 1999-12-29
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 53106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-034-650-10

Query Match 30.7%; Score 307.2; DB 13; Length 53106;
Best Local Similarity 77.7%; Pred. No. 2.8e-66;
Matches 408; Conservative 0; Mismatches 114; Indels 3; Gaps 3;
QY 69 AAAAAATTAATGGAATAGCTAGGCGGGTGGCTCAGCGCTGTAAATCCAGCACTTTA 128
Db |||||
QY 4598 AACCAAAAGACATCTCTGGGATGGGACAGGTGGCTCATGCTATATCCCAACATTTG 4657
Db |||||
QY 129 GAAGTCGAGAGGTGATCAGCTTGAAGTCAGGATTTTGAACAGAGCTGGGCAAC 188
Db |||||
QY 4658 GGAGCTGAGTGGGTTGATCACTTGAAGTCAGGAG-TTTGAACAGAGCTGGCAACAT 4716
Db |||||
QY 189 GGTGAACCCCATCTCTACTAAAAATA-AAAAATTTAGCTNGGGTGGGTGCTCACCT 247
Db |||||
QY 4717 GTTGAACCCCATCTCTACTAAAAACACAAAAATTTAGTGGGCATGGTGGCTCATCC 4776
Db |||||
QY 248 GTATATCCAGCACTTTGGGAGGTGAGACGGGTGGATCACTGAAGTCAGGAGTTCAAGG 307
Db |||||
QY 4777 GTAATCCAGCACTTTGGGAGGTGGGAGGAGGTGGATCACTTAAGTCAGAGTTCCAGA 4836
Db |||||
QY 308 CCAGCTGGGCAACATGCTGAACCCAGCTCTCTACTAAAAATACAAAAATTTAGCCAGTG 367
Db |||||
QY 4837 GCAGTCTGGGCAACATGCTGAACCCCATCTCTATTTAAAAATACAAAAATTTAGTCGG 4896
Db |||||
QY 368 TGGTGGCAGACGCTGTAGTCCAGCTACTTGGGAGGTGAGCGGAGAGATCCCTTGA 427
Db |||||
QY 4897 TGGTGGCAGCTCTCTGTAGTCCCGGCTTCTCAGGAGGTGAGGAGGAGATCACTTTGA 4956
Db |||||

QY 428 CCCAGTAGGACAGAGTTCAGCTAGGCGGAGATAAGAGTCACTGCACTCCAGCTGGGTGA 487
Db |||||
QY 4957 CCCAGTAGGCGGAGGTTCAGCTAGTCAAGAT-ACTGCCACTGCATCCAGCTGGGAA 5015
Db |||||
QY 488 CAGAGCAGAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATA 547
Db |||||
QY 5016 CAGAGGAGAGCTCCCTCTCAAAAATAAATAAACAATAAATAAATAAATAAATAAATA 5075
Db |||||
QY 548 TAAATAAATAATCTAAAGAGGCTGGCATTTGCTTAGCACTTATAT 592
Db |||||
QY 5076 AATAAATAAATAATAGCTGGGCAATGCTGTGTGCTGTAAATCT 5120
Db |||||

RESULT 10
US-09-967-768A-314/c
; Sequence 314, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 314
; LENGTH: 174424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-314

Query Match 30.7%; Score 307; DB 10; Length 174424;
Best Local Similarity 83.1%; Pred. No. 5.5e-66;
Matches 409; Conservative 0; Mismatches 76; Indels 7; Gaps 5;
QY 76 TTAATGAATAGCTAGGCGGGTGGCTCAGCGCTGTAAATCCAGCACTTTAGAGGTC 135
Db |||||
QY 132168 TAAAAAATAAAGAGCTAGGCGAGTGGCTCACACCTATATCTTAGCACTTTGGGAGGC 132109
Db |||||
QY 136 GAAGAGGTGGATCACTTCAGCTCAGGAGTTTGTAGACCCAGCTGGCCACACAGCTGAAA 195
Db |||||
QY 132108 GAGGAGGTGGATCACTTCAGCTCAGGAG-TTTGAACCCAGCTTAGCAATGTGGTAAA 132050
Db |||||
QY 196 CCCATCTCTACTAAAAAT-AAAAATTTAGCTNGGGTGGGTGCTCACACCTGTAAAT 252
Db |||||
QY 132049 CCCCCTCTCTACCAAAAAATACAAAAAATTTAGCCGGGACGCTGGCTCAGCTTAAAT 131990
Db |||||
QY 253 CCCAGCACTTTGGAGGCTGAGACGGGTGGATCACTGAAGTCAGGAGTTCAAGGCCAGC 312
Db |||||
QY 131989 CCCAACCTTTGGGAGGAGGAGGCGGTGGATCACTTCAGGTCAGGAGTTCCAGACCACT 131930
Db |||||
QY 313 CTGGGCAACATGCTGAACACAGCTCTCTACTAAAA-ATACAAAAATTTAGCCAGGTGGT 371
Db |||||
QY 131929 CTGGCCACATGCTGAACCCCTGTCTCTACAAAAATACAAAAATTTAGCCAGGCGTGGT 131870
Db |||||
QY 372 GGCACAGCTGTAGTCCAGCTACTTTGGAGGCTGAGCGGAGAGATCGCTTGAACCCA 431
Db |||||
QY 131869 GCGCAGCGCTGTAAATCCAGCTACTTTGGAGGCTGAGCGGAGAGATTTGCTTGAACCA 131810
Db |||||
QY 432 GTAGCAGAGTTGACAGTGCAGCCAGATAGAGTCACTGCACCTCCAGCTGGGTGAAGA 491
Db |||||
QY 131809 GGAGCAGAGTTGACAGTGCAGCCAGAT-CGTGCCATTTGACCTCCAGCTGGGCGGAGA 131751
Db |||||
QY 492 GCAAGACTCCCTCTCAG-AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 550
Db |||||

Query Match 30.4%; Score 304.2; DB 13; Length 113000;
 Best Local Similarity 81.2%; Pred. No. 2.3e-65;
 Matches 377; Conservative 0; Mismatches 84; Indels 3; Gaps 2;

QY 71 AAAAAATTAATGAATAGCTAGGCGGCTGCTCAGCGCTGTAATCCAGCACTTTAGA 130
 DB 11101 AATATATATATAGTTGGCCAGGCACAGTGGCAAGCGCTGTAATCCAGCACTTTGGG 11042

QY 131 AGTTCGAGAGGGTGGATCACTTTGAGTTCAGAGTCTTTGAGACCAAGCCTGCCAACAACGG 190
 DB 11041 AGGCTGAGCAGGTGAATCACTGAGCTCAGGA-ATTGAGACCAAGCCTGCCAACAATGG 10983

QY 191 TGAACCCCATCTCTACTATAAATAAATAAATTTAGCTNGGCTGGCTCACAACCTGTA 250
 DB 10982 TGAACCCCATCTCTACTATAAATAAATAAATTTAGCCAGGCACAGTGGCTCAGCGCTGC 10923

QY 251 ATCCAGCACTTTGGAGGCTGAGACGGGTGATCACTGAGTCAAGTTCAGGCCA 310
 DB 10922 ATCCAGCACTTTGGAGGCTGAGTGGGCGATCACTGATGTGAGAGTTCGAGATCA 10863

QY 311 GCTGGGCAATAGTGTGAACCAACGCTCTCTACTATAAATAAATAAATTTAGCCAGGTGG 370
 DB 10862 GCTGGGCAATAGTGTGAACCAACGCTCTCTACTATAAATAAATAAATTTAGCCAGGTGG 10803

QY 371 TGGCACAAGCCTGTAGTCCAGCTACTTTGGAGGCTGAGCGGAGAGTATCGTTGAACCC 430
 DB 10802 TGACGGCTCTCTGTAATCCAGCTACTCGGAGACTGAGGAGGAGATTCCTTGAACCC 10743

QY 431 AGTGGCAGAGGTTGCACTGAGCGGAGATAGAGTCACTGCACTCCAGCTGGGTGACAG 490
 DB 10742 AGGAGCGGAGTTGCACTGAGCGGAGATAGAGTCACTGCACTCCAGCTGGGTGACAG 10685

QY 491 AGCAAGATCTCCTCTCGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 534
 DB 10684 AGCAAGATCTCCTCTCGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 10641

RESULT 13
 US-10-292-798-1279/c
 ; Sequence 1279, Application US/10292798
 ; Publication No. US20030235833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUWA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/166
 ; CURRENT APPLICATION NUMBER: US/10/292,798
 ; PRIOR FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 10/017,161
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001-246789
 ; NUMBER OF SEQ ID NOS: 2070
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1279
 ; LENGTH: 27087
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; LOCATION: source
 ; FEATURE:
 ; LOCATION: (1) .. (27087)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (201) .. (498)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (834) .. (923)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7389) .. (7511)
 ; FEATURE:

FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (10905) .. (11021)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (13053) .. (13140)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (19148) .. (19452)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (26643) .. (26887)
 ; US-10-292-798-1279

Query Match 30.3%; Score 303.4; DB 12; Length 27087;
 Best Local Similarity 82.5%; Pred. No. 1.9e-65;
 Matches 383; Conservative 0; Mismatches 77; Indels 4; Gaps 3;

QY 86 TAGCTAGGCGGGTGGCTCAGCGCTGTAATCCAGCACTTTAGAGGTTGAAAGAGGGTG 145
 DB 8635 TGGGCCAGGTGGGTGGCGCCAGCGCTGTAATCCAGCACTTTGGGAGGCTTAGAGGGCG 8576

QY 146 GATCACTTGAAGTTCAGGAGTTTGGAGCAGCCTGGCCACACAGCGTGAACCCCATCTCT 205
 DB 8575 GATCACTTGAAGTTCAGGAGTTTGGAGCAGCCTGGCCACACAGCGTGAACCCCATCTCT 8517

QY 206 ACTAAAAATAAATAAATTTAGCTNGGCTGGGTGGCTCAGCTGTATCCAGCACTTTGG 265
 DB 8516 ACTAAAAATAAATAAATTTAGCTNGGCTGGGTGGCTCAGCTGTATCCAGCACTTTGG 8457

QY 266 GAGGCTGAGACGGGTGGCTCAGCTGAGTCAAGTTCAGGAGTTTCAAGGCCAGCTGGGCAACATGG 325
 DB 8456 GAGGCTGAGACGGGTGGCTCAGCTGAGTCAAGTTCAGGAGTTTCAAGGCCAGCTGGGCAACATGG 8399

QY 326 TGAACCAAGTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 385
 DB 8398 GGAACCCCGTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 8339

QY 386 GTCCAGCTACTTTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTTCAGGAGGTTG 445
 DB 8338 GTCCAGCTACTTTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTTCAGGAGGTTG 8279

QY 446 CAGTGGCGGAGATGAGTCACTGCTCAGCTCCAGCTGGGTGACAGCAAGCAAGTCCCTCT 505
 DB 8278 CAGTGGCGGAGATGAGTCACTGCTCAGCTCCAGCTGGGTGACAGCAAGCAAGTCCCTCT 8220

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 549
 DB 8219 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 8176

RESULT 14
 US-10-017-161-1605/c
 ; Sequence 1605, Application US/10017161
 ; Publication No. US20030143668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUWA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: NOVEL G PROTEIN- COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/0152
 ; CURRENT APPLICATION NUMBER: US/10/017,161
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001/246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2430
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1605
 ; LENGTH: 27087
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

NAME/KEY: source
LOCATION: (1)...(27087)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)...(498)
FEATURE:
NAME/KEY: CDS
LOCATION: (834)...(923)
FEATURE:
NAME/KEY: CDS
LOCATION: (7389)...(7511)
FEATURE:
NAME/KEY: CDS
LOCATION: (10905)...(11021)
FEATURE:
NAME/KEY: CDS
LOCATION: (13053)...(13140)
FEATURE:
NAME/KEY: CDS
LOCATION: (19148)...(19452)
FEATURE:
NAME/KEY: CDS
LOCATION: (26643)...(26887)
US-10-017-161-1605

Query Match
Best Local Similarity 30.3%; Score 303.4; DB 13; Length 27087;
Matches 383; Conservative 0; Mismatches 77; Indels 4; Gaps 3;

QY 86 TAGCTAGGCGGGTGGCTCAGCGCTGTAATCCAGCACTTTAGAGAGTTCGAGAGGGTG 145
Db 8635 TGGCCAGGTGGGGTGGCCAGCGCTGTAATCCAGCACTTTGGAGGGCTAGGAGGGG 8576

QY 146 GATCACTTAGGTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 205
Db 8575 GATCACTTAGGTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 8517

QY 206 ACTAAAAATAAAAAATTAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 265
Db 8516 ACTAAAAATAAAAAATTAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 8457

QY 266 GAGCTTGAGACGGGTGGATCACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 325
Db 8456 GAGCGGAGGCGAGGAGATCA--TGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 8399

QY 326 TGAAACACGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 385
Db 8398 GGAACCCCGTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 8339

QY 386 GTCCAGCTACTTGGAGGCTGAGGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGT 445
Db 8338 GTCCAGATCTCAGGAGGTTGAGGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGG 8279

QY 446 CAGTGAAGGAGATGAAGTCACTGCACTCCAGCGTGGTGGTGGTGGTGGTGGTGGTGG 505
Db 8278 CAGTGAAGGAGAT--AGCTCCACTGCTCCAGCGTGGTGGTGGTGGTGGTGGTGGTGG 8220

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 549
Db 8219 CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 8176

RESULT 15
US-09-967-768A-314
Sequence 314, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO 314
LENGTH: 174424
TYPE: DNA
ORGANISM: Homo sapiens
US-09-967-768A-314

Query Match
Best Local Similarity 30.1%; Score 301.4; DB 10; Length 174424;
Matches 397; Conservative 0; Mismatches 82; Indels 7; Gaps 4;

QY 70 AAAAAATTAAATGGAATAGGCTAGGCGGGTGGCTCAGCGCTGTAAATCCAGCACTTTAG 129
Db 69715 AAAAAATAAATGGAATAGGCTAGGCGGGTGGCTCAGCGCTGTAAATCCAGCACTTTAG 69774

QY 130 AAGGTCGAAGAGGGTGGATCACTTGAAGTCAGGAGTTTGAAGCAGCAGCTGGCCACACG 189
Db 69775 GAGGTCGAAGCAGCAGATCACTTGAAGTCAGGAG--TTCGAGACAGCCTGGCCACATG 69833

QY 190 GTGAACCCCATCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 246
Db 69834 GTGAACCCCTGTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 69893

QY 247 TGTAAATCCAGCACTTTGGAGGGTGGAGCGGTGGATCACTTGAAGTCAGGAGTTCAAG 306
Db 69894 TGTAAATCCAGCACTTTGGAGGGTGGAGCGGTGGATCACTTGAAGTCAGGAGTTCAAG 69953

QY 307 GCCAGCTGGGCAACATGGTGAACACCACTGCTCTACTTAAATAAATAAATAAATAAATA 366
Db 69954 ACCAGCTGGCAACATGGTGAACACCACTGCTCTACTTAAATAAATAAATAAATAAATA 70013

QY 367 GTGGTGGCACAACCGCTGTAGTCCAGCACTTGGAGGCTGAGCGGAGAAATCGCTTGA 426
Db 70014 GTGGTGGGCGCACTGTAGTCCAGCACTTGGAGGCTGAGCGGAGAAATCGCTTGA 70073

QY 427 ACCCAGTAGGCGAGGTTGCACTGAGCGGAGATGAAGTCACTGCACTCCAGCTGGGTG 486
Db 70074 ACCTGGGAGCAGAGGTTGCACTGAGCGGAGCAT--TGCCCACTGCACTTGGGTG 70132

QY 487 ACAGAGCAAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAA 546
Db 70133 ACAGAGAAAGAGTCTGTCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATA 70190

QY 547 AATAAA 552
Db 70191 TAAAAA 70196

Search completed: January 31, 2004, 17:25:56
Job time : 355 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:18:36 ; Search time 38.5 Seconds
(without alignments)
286.612 Million cell updates/sec

Title: US-09-784-423-124

Perfect score: 25

Sequence: 1 GGTTCAGTGAGCCGAGATAAGAGT 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/2/ina/ptotus COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	3	US-09-018-584A-124
2	25	100.0	1000	3	US-09-018-584A-32
3	20	80.0	764	4	US-09-288-143-57
4	20	80.0	1875	2	US-08-683-743-3
5	20	80.0	4042	3	US-08-406-030A-17
6	20	80.0	4129	2	US-08-370-319C-12
7	20	80.0	4129	3	US-09-224-834-12
8	20	80.0	45716	4	US-08-965-048-5
9	20	80.0	45989	4	US-08-965-048-6
10	19	76.0	21	1	US-08-133-623-2
11	19	76.0	239	2	US-08-687-080-93
12	19	76.0	265	2	US-08-849-701-1
13	19	76.0	283	4	US-08-579-445-26
14	19	76.0	294	2	US-08-481-658B-61
15	19	76.0	294	2	US-08-477-504A-61
16	19	76.0	294	2	US-08-486-756A-61
17	19	76.0	294	2	US-08-485-862B-61
18	19	76.0	294	3	US-08-787-739-61
19	19	76.0	294	3	US-08-487-077A-61
20	19	76.0	294	3	US-08-485-863A-61
21	19	76.0	294	3	US-08-485-049D-61
22	19	76.0	294	3	US-09-178-115-61
23	19	76.0	294	3	US-09-177-776-61
24	19	76.0	302	2	US-08-849-701-3
25	19	76.0	308	4	US-09-702-705-1111
26	19	76.0	308	4	US-09-736-457-1111
27	19	76.0	336	3	US-09-385-982-17

c 28 19 76.0 363 4 US-09-702-705-878 Sequence 878, App
c 29 19 76.0 363 4 US-09-736-457-878 Sequence 878, App
c 30 19 76.0 364 4 US-09-702-705-867 Sequence 867, App
c 31 19 76.0 364 4 US-09-736-457-867 Sequence 867, App
32 19 76.0 367 4 US-09-702-705-1143 Sequence 1143, Ap
33 19 76.0 367 4 US-09-702-705-1626 Sequence 1626, Ap
34 19 76.0 367 4 US-09-736-457-1143 Sequence 1143, Ap
35 19 76.0 367 4 US-09-736-457-1626 Sequence 1626, Ap
c 36 19 76.0 368 4 US-09-702-705-1003 Sequence 1003, Ap
37 19 76.0 368 4 US-09-702-705-1038 Sequence 1038, Ap
c 38 19 76.0 368 4 US-09-702-705-1044 Sequence 1044, Ap
c 39 19 76.0 368 4 US-09-702-705-1092 Sequence 1092, Ap
c 40 19 76.0 368 4 US-09-702-705-1584 Sequence 1584, Ap
c 41 19 76.0 368 4 US-09-736-457-1003 Sequence 1003, Ap
c 42 19 76.0 368 4 US-09-736-457-1038 Sequence 1038, Ap
c 43 19 76.0 368 4 US-09-736-457-1044 Sequence 1044, Ap
c 44 19 76.0 368 4 US-09-736-457-1092 Sequence 1092, Ap
c 45 19 76.0 368 4 US-09-736-457-1584 Sequence 1584, Ap

ALIGNMENTS

RESULT 1
US-09-018-584A-124
; Sequence 124, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; FILING DATE: 04-Feb-1998
; APPLICATION NUMBER: US/09/018,584A
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026,9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-3501
; INFORMATION FOR SEQ ID NO: 124:
; LENGTH: 25
; SEQUENCE CHARACTERISTICS:
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-018-584A-124

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 5,7e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGTTCAGTGAGCCGAGATAAGAGT 25
Db 1 GGTTCAGTGAGCCGAGATAAGAGT 25

RESULT 2

US-09-018-584A-32
 ; Sequence 32, Application US/09018584A
 ; Patent No. 6238863
 ; GENERAL INFORMATION:
 ; APPLICANT: Schumm, James W.
 ; APPLICANT: Bacher, Jeffery W.
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR
 ; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
 ; REPEAT DNA MARKERS
 ; NUMBER OF SEQUENCES: 147
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Promega Corporation
 ; STREET: 2800 Woods Hollow Road
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: U.S.A.
 ; ZIP: 53711-5399
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
 ; COMPUTER: IBM compatible PC
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Word 97 (DOS text format)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/018,584A
 ; FILING DATE: 04-Feb-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Grady J. Frenchick
 ; REGISTRATION NUMBER: 29,018
 ; REFERENCE/DOCKET NUMBER: 16026.9180
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 257-3501
 ; TELEFAX: (608) 257-2275
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1000 bp
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Double
 ; TOPOLOGY: Circular
 ; MOLECULE TYPE: Genomic DNA
 ; HYPOTHETICAL: no
 ; IMMEDIATE SOURCE:
 ; CLONE: S132
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT: 22
 ; US-09-018-584A-32

Query Match 100.0%; Score 25; DB 3; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATAAGT 25

Db 441 GGTTCAGTGCAGCGAGATAAGT 465

RESULT 3

US-09-288-143-57
 ; Sequence 57, Application US/09288143
 ; Patent No. 6433139
 ; GENERAL INFORMATION:
 ; APPLICANT: Brewer et al.
 ; TITLE OF INVENTION: 53 Human Secreted Proteins
 ; FILE REFERENCE: P2018P1
 ; CURRENT APPLICATION NUMBER: US/09/288,143
 ; CURRENT FILING DATE: 1999-04-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/21142
 ; EARLIER FILING DATE: 1998-10-08
 ; EARLIER APPLICATION NUMBER: 60/061,463
 ; EARLIER FILING DATE: 1997-10-09
 ; EARLIER APPLICATION NUMBER: 60/061,529

; EARLIER FILING DATE: 1997-10-09
 ; EARLIER APPLICATION NUMBER: 60/071,498
 ; EARLIER FILING DATE: 1997-10-09
 ; EARLIER APPLICATION NUMBER: 60/061,527
 ; EARLIER FILING DATE: 1997-10-09
 ; EARLIER APPLICATION NUMBER: 60/061,536
 ; EARLIER FILING DATE: 1997-10-09
 ; EARLIER APPLICATION NUMBER: 60/061,532
 ; EARLIER FILING DATE: 1997-10-09
 ; NUMBER OF SEQ ID NOS: 219
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 57
 ; LENGTH: 764
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-288-143-57

Query Match 80.0%; Score 20; DB 4; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATA 20

Db 674 GGTTCAGTGCAGCGAGATA 693

RESULT 4

US-08-683-743-3
 ; Sequence 3, Application US/08683743
 ; Patent No. 5843697
 ; GENERAL INFORMATION:
 ; APPLICANT: Pestka, Sidney
 ; APPLICANT: Kotsenko, Serguei
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
 ; TITLE OF INVENTION: CHAIN
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; STREET: Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/683,743
 ; FILING DATE: 17-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 601-1-050
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1875 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; US-08-683-743-3

Query Match 80.0%; Score 20; DB 2; Length 1875;
 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
DB 1551 GGTTCAGTGAGCCGAGATA 1570

RESULT 5

US-08-406-030A-17
; Sequence 17, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Hauge, Brian M.
; APPLICANT: Seldan, Richard F.
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4042 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-17

Query Match 80.0%; Score 20; DB 3; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
DB 2894 GGTTCAGTGAGCCGAGATA 2913

RESULT 6

US-08-370-319C-12
; Sequence 12, Application US/08370319C
; Patent No. 5856091
; GENERAL INFORMATION:
; APPLICANT: Brichard, Vincent; Van Pel, Aline;
; APPLICANT: Traversari, Catia; W lfel, Thomas;
; APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR PROCESSED TO AT LEAST ONE TUN
; TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,319C
; FILING DATE: 10-JANUARY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/272,351
; FILING DATE: 8-JULY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,978
; FILING DATE: 18-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5856091man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5377.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 638-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence is preceded by an
; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
; OTHER INFORMATION: kilobases
US-08-370-319C-12

Query Match 80.0%; Score 20; DB 2; Length 4129;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
DB 3066 GGTTCAGTGAGCCGAGATA 3085

RESULT 7

US-09-224-834-12
; Sequence 12, Application US/09224834
; Patent No. 6201111
; GENERAL INFORMATION:

APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W lfel, thomas; Coullie, Pierre;
APPLICANT: Boon-Falleur, Thierry; De plaen, Btienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6201111man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence is preceded by an
OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
OTHER INFORMATION: kilobases
US-09-224-834-12

Query Match 80.0%; Score 20; DB 3; Length 4129;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
DB 3066 GGTTCAGTGAGCCGAGATA 3085

RESULT 8
US-08-965-048-5
Sequence 5, Application US/08965048
Patent No. 6323244
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT APPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 45716

TYPE: DNA
ORGANISM: Homo sapiens
US-08-965-048-5

Query Match 80.0%; Score 20; DB 4; Length 45716;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
DB 33531 GGTTCAGTGAGCCGAGATA 33550

RESULT 9
US-08-965-048-6
Sequence 6, Application US/08965048
Patent No. 6323244
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT APPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 45989
TYPE: DNA
ORGANISM: Homo sapiens
US-08-965-048-6

Query Match 80.0%; Score 20; DB 4; Length 45989;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
DB 33645 GGTTCAGTGAGCCGAGATA 33664

RESULT 10
US-08-133-629-2
Sequence 2, Application US/08133629
Patent No. 5597694
GENERAL INFORMATION:
APPLICANT: Munroe, David J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,629
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greer, Helen
REGISTRATION NUMBER: 36,816
REFERENCE/DOCKET NUMBER: MC828/7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-133-629-2

Query Match 76.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
DB 3 GGTTCAGTGAGCCGAGAT 21

RESULT 11
US-08-687-080-93/c
; Sequence 93, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Denlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 5' END OF INTRON 16 OF RAD50 GENOMIC
INDIVIDUAL ISOLATE: SEQUENCE
US-08-687-080-93

Query Match 76.0%; Score 19; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||

Db 128 GGTTCAGTGAGCCGAGAT 110

RESULT 12
US-08-849-701-1
; Sequence 1, Application US/08849701
; Patent No. 5922544
; GENERAL INFORMATION:
; APPLICANT: Miyai, Kiyoshi
; APPLICANT: Naitoh, Tsutomu
; APPLICANT: Yonekawa, Yoshihiro
; TITLE OF INVENTION: Method of Cell Detection
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,701
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JF95/02734
FILING DATE: 27-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: EIKEN1.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other
IMMEDIATE SOURCE:
CLONE: A1u sequence BLUR8
US-08-849-701-1

Query Match 76.0%; Score 19; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||

Db 194 GGTTCAGTGAGCCGAGAT 212

RESULT 13
US-08-579-445-26
; Sequence 26, Application US/08579445
; Patent No. 6566053
; GENERAL INFORMATION:
; APPLICANT: Feruchio, Manuel
; APPLICANT: Peinado, Miguel A.
; APPLICANT: Ionov, Yuri
; APPLICANT: Malkhosyan, Sergei
; TITLE OF INVENTION: Identification of Neoplasms by Detection
; TITLE OF INVENTION: Identification of Neoplasms by Detection
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/579,445
APPLICATION NUMBER: US/08/579,445
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,484
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kirkpatrick, Anita M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: STRATAG.009A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-579-445-26

Query Match 76.0%; Score 19; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGAGCCGAGAT 19
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Db 218 GGTTCAGTGAGCCGAGAT 236

RESULT 14
US-08-481-658B-61/c
Sequence 61, Application US/08/481658B
Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-481-658B-61

Query Match 76.0%; Score 19; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGAGCCGAGAT 19
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Db 75 GGTTCAGTGAGCCGAGAT 57

RESULT 15
US-08-477-504A-61/c
Sequence 61, Application US/08/477504A
Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-477-504A-61

Query Match 76.0%; Score 19; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||
Db 75 GGTTCAGTGAGCCGAGAT 57
|||

Search completed: January 31, 2004, 17:34:49
Job time : 39.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:19:57 ; Search time 143 Seconds
(without alignments)
637.160 Million cell updates/sec

Title: US-09-784-423-124

Perfect score: 25

Sequence: 1 GGTTCAGTGCAGCCGAGATAGAGT 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2434939 seqs, 1822278265 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Published Applications NA.*
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11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	9	US-09-784-423-124
2	25	100.0	1000	9	Sequence 124, App
3	21	84.0	611	13	Sequence 32, Appl
4	21	84.0	611	14	Sequence 256, App
5	21	84.0	619	13	Sequence 256, App
6	21	84.0	619	13	Sequence 256, App
7	21	84.0	619	13	Sequence 256, App
8	21	84.0	619	13	Sequence 256, App
9	21	84.0	619	13	Sequence 256, App
10	21	84.0	619	13	Sequence 256, App
11	21	84.0	619	13	Sequence 256, App
12	21	84.0	619	13	Sequence 256, App
13	21	84.0	619	13	Sequence 256, App
14	21	84.0	619	13	Sequence 256, App
15	21	84.0	619	13	Sequence 256, App
16	21	84.0	619	13	Sequence 256, App
17	21	84.0	619	13	Sequence 256, App
18	21	84.0	619	13	Sequence 256, App

Sequence 41283, A
Sequence 128887, A
Sequence 128887, A
Sequence 166508, A
Sequence 166508, A
Sequence 102290, A
Sequence 102290, A
Sequence 102290, A
Sequence 102290, A
Sequence 102290, A
Sequence 5690, Ap
Sequence 4, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 27530, A
Sequence 138166, A
Sequence 138166, A
Sequence 2157, Ap
Sequence 8428, Ap
Sequence 148, App
Sequence 66429, A
Sequence 66429, A
Sequence 762, App
Sequence 26090, A
Sequence 91667, A
Sequence 91667, A
Sequence 91667, A
Sequence 91667, A
Sequence 291649, A
Sequence 291649, A
Sequence 281502, A

ALIGNMENTS

RESULT 1

US-09-784-423-124

Sequence 124, Application US/09784423

Patent No. US20020012924A1

GENERAL INFORMATION:

APPLICANT: Schumm, James W.

Bachner, Jeffery W.

TITLE OF INVENTION: MATERIALS AND METHODS FOR

IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSER: Promega Corporation

STREET: 2800 Woods Hollow Road

CITY: Madison

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53711-5399

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

COMPUTER: IBM compatible PC

OPERATING SYSTEM: Windows 95

SOFTWARE: Word 97 (DOS text format)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784.423

FILING DATE: 15-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/018.584

FILING DATE: 04-Feb-1998

ATTORNEY/AGENT INFORMATION:

NAME: Grady J. Frenchick

REGISTRATION NUMBER: 29,018

REFERENCE/DOCKET NUMBER: 16026.9180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 257-3501

TELEFAX: (608) 257-2275

INFORMATION FOR SEQ ID NO: 124

```

;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 25
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 124
US-09-784-423-124

Query Match      100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GGTTCAGTGAGCCGAGATAGAGT 25
        |||||
Db      1 GGTTCAGTGAGCCGAGATAGAGT 25

RESULT 2
US-09-784-423-32
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
;   APPLICANT: Schumm, James W.
;           Bacher, Jeffrey W.
;
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
;
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Promega Corporation
;   STREET: 2800 Woods Hollow Road
;   CITY: Madison
;   STATE: Wisconsin
;   COUNTRY: U.S.A.
;   ZIP: 53711-5399
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
;   COMPUTER: IBM compatible PC
;   OPERATING SYSTEM: Windows 95
;   SOFTWARE: Word 97 (DOS text format)
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/784,423
;   FILING DATE: 15-Feb-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/018,584
;     FILING DATE: 04-Feb-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Grady J. Frenchick
;     REGISTRATION NUMBER: 29,018
;     REFERENCE/DOCKET NUMBER: 16026.9180
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (608) 257-3501
;     TELEFAX: (608) 257-2275
;
; INFORMATION FOR SEQ ID NO: 32
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1000 bp
;     TYPE: Nucleic Acid
;     STRANDEDNESS: Double
;     TOPOLOGY: Circular
;     MOLECULE TYPE: Genomic DNA
;     HYPOTHETICAL: no
;     IMMEDIATE SOURCE:
;       CLONE: SI32
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT: 22
;   SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      100.0%; Score 25; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SEQ ID NO 256
LENGTH: 611
TYPE: DNA
ORGANISM: Human
US-10-027-632-256

Query Match 84.0%; Score 21; DB 14; Length 611;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||
DB 343 GGTTCAGTGGCCGAGATAA 363

RESULT 5

US-10-027-632-76653/c
; Sequence 76653, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76653
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-76653

Query Match 84.0%; Score 21; DB 13; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||
DB 95 GGTTCAGTGGCCGAGATAA 75

RESULT 6

US-10-027-632-76654/c
; Sequence 76654, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76654
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-76654

Query Match 84.0%; Score 21; DB 13; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||
DB 95 GGTTCAGTGGCCGAGATAA 75

RESULT 7

US-10-027-632-109145/c
; Sequence 109145, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109145
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109145

Query Match 84.0%; Score 21; DB 13; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCCGAGATAA 75

RESULT 8

US-10-027-632-109146/c
 ; Sequence 109146, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 109146
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(619)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-109146

Query Match 84.0%; Score 21; DB 13; Length 619;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCCGAGATAA 75

RESULT 9

US-10-027-632-76653/c
 ; Sequence 76653, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76653
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(619)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-76653

Query Match 84.0%; Score 21; DB 14; Length 619;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCCGAGATAA 75

RESULT 10

US-10-027-632-76654/c
 ; Sequence 76654, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76654
 ; LENGTH: 619
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(619)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-76654

Query Match 84.0%; Score 21; DB 14; Length 619;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 Db 95 GGTTCAGTGCAGCCGAGATAA 75

RESULT 11

US-10-027-632-109145/c
 ; Sequence 109145, Application US/10027632

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109145
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109145
```

```
Query Match      84.0%; Score 21; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 GGTTCAGTGCAGCCGAGATAA 21
          |||||
Db      95 GGTTCAGTGCAGCCGAGATAA 75
```

```
RESULT 12
US-10-027-632-109146/c
; Sequence 109146, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109146
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109146
```

```
Query Match      84.0%; Score 21; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GGTTCAGTGCAGCCGAGATAA 21
          |||||
Db      95 GGTTCAGTGCAGCCGAGATAA 75
```

```
RESULT 13
US-10-027-632-41282/c
; Sequence 41282, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41282
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41282
```

```
Query Match      84.0%; Score 21; DB 13; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 GGTTCAGTGCAGCCGAGATAA 21
          |||||
Db      112 GGTTCAGTGCAGCCGAGATAA 92
```

```
RESULT 14
US-10-027-632-41283/c
; Sequence 41283, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
```

; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41283
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41283

Query Match 84.0%; Score 21; DB 13; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTGCAGTGAGCCGAGATAA 21
|||||
Db 112 GGTTGCAGTGAGCCGAGATAA 92

RESULT 15
US-10-027-632-41282/c
; Sequence 41282, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41282
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-41282

Query Match 84.0%; Score 21; DB 14; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTGCAGTGAGCCGAGATAA 21
|||||
Db 112 GGTTGCAGTGAGCCGAGATAA 92

Search completed: January 31, 2004, 17:39:48
Job time : 145 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:18:36 ; Search time 38.5 Seconds
(without alignments)
286.612 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TGTCCAGGACCAAGAAATTACAG 25

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3	US-09-018-584A-125
2	25	100.0	1000	3	US-09-018-584A-32
3	15	60.0	28720	4	US-09-341-587-7
4	14	56.0	627	4	US-08-981-030-2
5	14	56.0	627	4	US-08-981-030-12
6	14	56.0	682	4	US-08-981-030-1
7	14	56.0	1727	1	US-08-289-458-3
8	14	56.0	1727	2	US-08-761-549-3
9	14	56.0	4376	1	US-08-119-125A-1
10	14	56.0	6744	1	US-08-119-125A-2
11	14	56.0	9493	2	US-08-639-857-23
12	14	56.0	9493	4	US-08-469-260A-163
13	14	56.0	9493	4	US-08-488-446-163
14	14	56.0	9493	4	US-08-467-344A-163
15	14	56.0	99500	4	US-09-798-096-10
16	14	56.0	1230025	4	US-09-198-452A-1
17	14	56.0	22	2	US-08-332-766A-76
18	13	52.0	22	2	US-08-229-279-6
19	13	52.0	56	1	US-08-701-269-6
20	13	52.0	56	1	US-09-511-625B-57
21	13	52.0	89	4	US-09-084-120-23
22	13	52.0	91	3	US-08-332-766A-16
23	13	52.0	445	2	US-09-252-991A-15529
24	13	52.0	558	4	US-09-328-111-416
25	13	52.0	611	3	US-09-669-751-62
26	13	52.0	628	4	US-08-998-416-77
27	13	52.0	646	3	US-08-998-416-77

28	13	52.0	660	4	US-09-107-532A-1545
C 29	13	52.0	691	2	US-08-365-488A-29
C 30	13	52.0	691	3	US-08-880-342-29
31	13	52.0	700	3	US-08-991-789A-174
32	13	52.0	700	4	US-09-062-451-174
33	13	52.0	700	4	US-09-598-326-174
34	13	52.0	700	4	US-09-289-198-174
35	13	52.0	829	3	US-08-961-083-133
36	13	52.0	829	3	US-09-536-784-133
37	13	52.0	831	4	US-09-252-991A-15309
C 38	13	52.0	836	1	US-08-554-612C-26
39	13	52.0	881	4	US-09-482-273-40
C 40	13	52.0	932	1	US-08-554-612C-20
C 41	13	52.0	1001	4	US-09-641-638-514
C 42	13	52.0	1001	4	US-09-641-638-514
C 43	13	52.0	1001	4	US-09-641-638-516
C 44	13	52.0	1007	1	US-08-554-612C-17
C 45	13	52.0	1007	1	US-08-554-612C-18

ALIGNMENTS

RESULT 1

US-09-018-584A-125
Sequence 125, Application US/09018584A
Patent No. 6238863
GENERAL INFORMATION:
APPLICANT: Schuma, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
TITLE OF INVENTION: REPEAT DNA MARKERS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
CITY: Madison
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53711-5399

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
FILING DATE: 04-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026,9180
TELEPHONE: (608) 257-3501
TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-018-584A-125

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGTCCAGGACCAAGAAATTACAG 25

Db 1 TGTCCAGGACCAAGAAATTACAG 25

```
RESULT 2
US-09-018-584A-32/c
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bachner, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; US-09-018-584A-32

Query Match 100.0%; Score 25; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
Db 726 TGTGCCAGGACCAAGAAATTACAG 702

RESULT 3
US-09-341-587-7
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

Query Match 100.0%; Score 25; DB 3; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
Db 726 TGTGCCAGGACCAAGAAATTACAG 702

RESULT 4
US-08-981-030-2
; Sequence 2, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011
; FILING DATE: 12-JUN-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus pahari
; US-08-981-030-2

Query Match 56.0%; Score 14; DB 4; Length 627;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTACAA 24
Db 542 ACCAGAAATTACAA 555

RESULT 5
US-08-981-030-12
; Sequence 12, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011
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; FILING DATE: 12-JUN-1996
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 627 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rattus norvegicus
 ; US-08-981-030-12

Query Match 56.0%; Score 14; DB 4; Length 627;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTTCAC 24
 |||||
 Db 542 ACCAGAAATTTCAC 555

RESULT 6

US-08-981-030-1
 ; Sequence 1, Application US/08981030
 ; Patent No. 6447783
 ; GENERAL INFORMATION:

; APPLICANT:
 ; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
 ; NUMBER OF SEQUENCES: 13
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/981,030
 ; FILING DATE:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/IL96/00011
 ; FILING DATE: 12-JUN-1996

; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 682 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

US-08-981-030-1

Query Match 56.0%; Score 14; DB 4; Length 682;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTTCAC 24
 |||||
 Db 597 ACCAGAAATTTCAC 610

RESULT 7

US-08-289-458-3
 ; Sequence 3, Application US/08289458
 ; Patent No. 5608144
 ; GENERAL INFORMATION:

; APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
 ; APPLICANT: LEE, Kathleen Y.
 ; TITLE OF INVENTION: PLANT Gp2 PROMOTERS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: Stuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California

; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/289,458
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dow, Karen B.
 ; REGISTRATION NUMBER: 29,684
 ; REFERENCE/DOCKET NUMBER: 12176-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1727 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CAAT signal
 ; LOCATION: 1100..1103
 ; FEATURE:
 ; NAME/KEY: TATA signal
 ; LOCATION: 1139..1146
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1169
 ; OTHER INFORMATION: /note= "Transcriptional start site"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1172
 ; OTHER INFORMATION: /note= "pgp50 5' end"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1234..1236
 ; OTHER INFORMATION: /note= "Translation start codon"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1298
 ; OTHER INFORMATION: /note= "Intron start site"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..1233
 ; OTHER INFORMATION: /note= "Gp2 promoter sequence"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..1727
 ; OTHER INFORMATION: /note= "Gp2 Genomic DNA clone"
 ; US-08-289-458-3

Query Match 56.0%; Score 14; DB 1; Length 1727;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACACGAAATTT 21
 |||||
 Db 1619 GGAACACGAAATTT 1632

RESULT 8

US-08-761-549-3
 ; Sequence 3, Application US/08761549
 ; Patent No. 5981727
 ; GENERAL INFORMATION:
 ; APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
 ; APPLICANT: LEE, Kathleen Y.

```
;; TITLE OF INVENTION: PLANT Gp2 PROMOTERS AND USES THEREOF
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Khourie and Crew
;; STREET: Steuart Street Tower, One Market Plaza
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: US
;; ZIP: 94105-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/761,549
;; FILING DATE: 06-DEC-1996
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/289,458
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dow, Karen B.
;; REGISTRATION NUMBER: 29,684
;; REFERENCE/DOCKET NUMBER: 12176-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1727 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CAAT signal
;; LOCATION: 1100..1103
;; FEATURE:
;; NAME/KEY: TATA signal
;; LOCATION: 1139..1146
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1169-
;; OTHER INFORMATION: /note= "Transcriptional start site"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1172-
;; OTHER INFORMATION: /note= "pgp50 5' end"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1234..1236
;; OTHER INFORMATION: /note= "Translation start codon"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1298-
;; OTHER INFORMATION: /note= "Intron start site"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..1233
;; OTHER INFORMATION: /note= "Gp2 promoter sequence"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..1727
;; OTHER INFORMATION: /note= "Gp2 Genomic DNA clone"
;; US-08-761-549-3
Query Match 56.0%; Score 14; DB 2; Length 1727;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCAAGAAATTT 21
|||||
;;
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```
Db 1619 GGAACCAAGAAATTT 1632

RESULT 9
US-09-127-646-3
; Sequence 3, Application US/09127646
; Patent No. 6291744
; GENERAL INFORMATION:
; APPLICANT: Baden, Catherine S.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Lee, Kathleen Y.
; APPLICANT: DNA Plant Technology Corporation
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Group 2 Proteins and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 012176-004020US
; CURRENT APPLICATION NUMBER: US/09/127,646
; CURRENT FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 08/289,458
; EARLIER FILING DATE: 1994-08-12
; EARLIER APPLICATION NUMBER: US 08/761,549
; EARLIER FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 1727
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1727)
; OTHER INFORMATION: pepper plant Group 2 (Gp2) genomic DNA clone
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1233)
; OTHER INFORMATION: Gp2 promoter sequence
; FEATURE:
; NAME/KEY: CAAT signal
; LOCATION: (1100)..(1103)
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: (1139)..(1146)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1169)
; OTHER INFORMATION: transcriptional start site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1172)
; OTHER INFORMATION: pgp50 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1234)..(1236)
; OTHER INFORMATION: translation start codon
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1298)
; OTHER INFORMATION: intron start site
; US-09-127-646-3

Query Match 56.0%; Score 14; DB 3; Length 1727;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCAAGAAATTT 21
|||||
Db 1619 GGAACCAAGAAATTT 1632

RESULT 10
US-08-119-125A-1
; Sequence 1, Application US/08119125A
; Patent No. 5610011
; GENERAL INFORMATION:
```

APPLICANT: SMITH, Hilda Elizabeth
APPLICANT: VECHT, Uri
TITLE OF INVENTION: DNA Sequences which code for Virulence
TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polyp
TITLE OF INVENTION: Antibodies derived therefrom and the use thereof for the diagn
TITLE OF INVENTION: Protection against infection by S. suis in mammals, including
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centraal Diergeneeskundig Instituut
STREET: Edelhertweg 15
CITY: PH Lelystad
STATE:
COUNTRY: The Netherlands
ZIP: NL-8219
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS v. 6.0
SOFTWARE: WordPerfect v. 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,125A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00054
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: NL 9100510
FILING DATE: 21-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Handal, Anthony H.
REGISTRATION NUMBER: 26275
REFERENCE/DOCKET NUMBER: SMITHHE119125
TELEPHONE: (203) 838-8589
TELEFAX: (203) 838-8794
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4376 base pairs
TYPE: Nucleic acid with corresponding amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Streptococcus suis type II (pathogenic)
FEATURE:
OTHER INFORMATION: Extracellular protein factor (EF) gene
NAME/KEY: promoter -35 region
LOCATION: bp 66 to 71
FEATURE:
NAME/KEY: promoter -10 region
LOCATION: bp 89 to 94
FEATURE:
NAME/KEY: promoter -35 region
LOCATION: bp 153 to 158
FEATURE:
NAME/KEY: promoter -10 region
LOCATION: bp 176 to 181
FEATURE:
NAME/KEY: ribosome binding site
LOCATION: bp 350 to 356
FEATURE:
NAME/KEY: signal peptide
LOCATION: bp 361 to 498
FEATURE:
NAME/KEY: mature peptide
LOCATION: bp 499 to 2890
FEATURE:
NAME/KEY: dyad symmetry regions
LOCATION: from bp 4186 to 4198 and from bp 4203 to 4215
FEATURE:
NAME/KEY: dyad symmetry regions
LOCATION: from bp 4243 to 4257 and from bp 4263 to 4276

US-08-119-125A-1

Query Match 56.0%; Score 14; DB 1; Length 4376;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAAT 19

Db 314 CAGGAACCAAGAAAT 327

RESULT 11

US-08-119-125A-2

; Sequence 2, Application US/08119125A

; Patent No. 5610011

; GENERAL INFORMATION:

; APPLICANT: SMITH, Hilda Elizabeth

; APPLICANT: VECHT, Uri

; TITLE OF INVENTION: DNA Sequences which code for Virulence

; TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polyp

; TITLE OF INVENTION: Antibodies derived therefrom and the use thereof for the diagn

; TITLE OF INVENTION: Protection against infection by S. suis in mammals, including ;

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Centraal Diergeneeskundig Instituut

; STREET: Edelhertweg 15

; CITY: PH Lelystad

; STATE:

; COUNTRY: The Netherlands

; ZIP: NL-8219

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS v. 6.0

; SOFTWARE: WordPerfect v. 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/119,125A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/NL92/00054

; FILING DATE: 19-MAR-1992

; APPLICATION NUMBER: NL 9100510

; FILING DATE: 21-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Handal, Anthony H.

; REGISTRATION NUMBER: 26275

; REFERENCE/DOCKET NUMBER: SMITHHE119125

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203) 838-8589

; TELEFAX: (203) 838-8794

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6744 base pairs

; TYPE: Nucleic acid with corresponding amino acids

; STRANDEDNESS: single stranded

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus suis type II (pathogenic)

; FEATURE:

; OTHER INFORMATION: Extracellular factor related protein (EF*) gene

; FEATURE:

; NAME/KEY: promoter -35 region

; LOCATION: bp 66 to 71

; FEATURE:

; NAME/KEY: promoter -10 region

; LOCATION: bp 89 to 94

; FEATURE:

; NAME/KEY: promoter -35 region

; LOCATION: bp 153 to 158

; FEATURE:

; NAME/KEY: promoter -10 region

; LOCATION: bp 4263 to 4276

LOCATION: bp 176 to 181
FEATURE: ribosome binding site
LOCATION: bp 350 to 356
FEATURE: signal peptide
LOCATION: bp 361 to 438
FEATURE: start of repetitive units RI-R11
LOCATION: bp 2869, 3097, 3292, 3520, 4087, 4381, 4609, 4837,
LOCATION: 5065, 5293, 5521;
FEATURE: start of repetitive Asn-Pro-Asn-Ieu sequences
LOCATION: bp 2932, 3160, 3355, 3583, 4150, 4444, 4672, 4900,
LOCATION: 5128, 5356, 5584;
FEATURE: dyad symmetry regions
LOCATION: from bp 6554 to 6566 and from bp 6571 to 6583
FEATURE: dyad symmetry regions
LOCATION: from bp 6611 to 6625 and from bp 6631 to 6644
US-08-119-125A-2

Query Match 56.0%; Score 14; DB 1; Length 6744;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAAT 19
|||||
DB 314 CAGGAACCAAGAAAT 327

RESULT 12
US-08-639-857-23
; Sequence 23, Application US/08639857
; Patent No. 5955318
; GENERAL INFORMATION:
; APPLICANT: Simons, J. N.
; APPLICANT: Desai, S. M.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING THE
; TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,857
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5793.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-0378
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-639-857-23

Query Match 56.0%; Score 14; DB 2; Length 9493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14
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DB 4037 TGTGCCAGGAACCA 4050

RESULT 13
US-08-469-260A-163
; Sequence 163, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-260A-163

Query Match 56.0%; Score 14; DB 4; Length 9493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14
|||||
DB 4037 TGTGCCAGGAACCA 4050

RESULT 14

US-08-488-446-163
; Sequence 163, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-488-446-163

Query Match 56.0%; Score 14; DB 4; Length 9493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14

Db 4037 TGTGCCAGGAACCA 4050

RESULT 15

US-08-467-344A-163
; Sequence 163, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY

ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 9493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-08-467-344A-163

Query Match 56.0%; Score 14; DB 4; Length 9493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14

Db 4037 TGTGCCAGGAACCA 4050

Search completed: January 31, 2004, 17:34:51
Job time : 40.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 17:19:57 ; Search time 143 Seconds
(without alignments)
637.160 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TGTCCGAGACAGAAATTTACAG 25

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2434939 seqs, 1822278265 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCT08_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	US-09-784-423-125	Sequence 125, App
2	25	100.0	1000	US-09-784-423-32	Sequence 32, App
3	17	68.0	624	US-10-027-632-311837	Sequence 311837, App
4	17	68.0	624	US-10-027-632-311837	Sequence 311837, App
5	17	68.0	7273	US-10-017-161-1629	Sequence 1629, App
6	16	64.0	442	US-09-864-761-11479	Sequence 11479, A
7	16	64.0	494	US-10-027-632-179918	Sequence 179918, A
8	16	64.0	494	US-10-027-632-179918	Sequence 179918, A
9	16	64.0	624	US-10-027-632-220234	Sequence 220234, App
10	16	64.0	624	US-10-027-632-220235	Sequence 220235, App
11	16	64.0	624	US-10-027-632-220234	Sequence 220234, App
12	16	64.0	624	US-10-027-632-220235	Sequence 220235, App
13	16	64.0	641	US-10-027-632-114443	Sequence 114443, App
14	16	64.0	641	US-10-027-632-114443	Sequence 114443, App
15	16	64.0	1630	US-10-027-632-253734	Sequence 253734, App

c	16	64.0	1630	14	US-10-027-632-253734	Sequence 253734, A
	17	64.0	1791	13	US-09-814-353-21503	Sequence 21503, A
	18	60.0	315	12	US-10-242-535A-25180	Sequence 25180, A
	19	60.0	538	13	US-10-027-632-81341	Sequence 81341, A
	20	60.0	538	13	US-10-027-632-82646	Sequence 82646, A
	21	60.0	538	13	US-10-027-632-180681	Sequence 180681, A
	22	60.0	538	13	US-10-027-632-301780	Sequence 301780, A
	23	60.0	538	14	US-10-027-632-81341	Sequence 81341, A
	24	60.0	538	14	US-10-027-632-82646	Sequence 82646, A
	25	60.0	538	14	US-10-027-632-180681	Sequence 180681, A
	26	60.0	538	14	US-10-027-632-301780	Sequence 301780, A
	27	60.0	548	13	US-10-027-632-66186	Sequence 66186, A
	28	60.0	548	13	US-10-027-632-299033	Sequence 299033, A
	29	60.0	548	14	US-10-027-632-66186	Sequence 66186, A
	30	60.0	548	14	US-10-027-632-299033	Sequence 299033, A
	31	60.0	569	10	US-09-917-800A-198	Sequence 198, App
	32	60.0	569	12	US-10-388-334-331	Sequence 331, App
	33	60.0	582	13	US-10-029-386-1285	Sequence 1285, App
	34	60.0	598	13	US-10-027-632-232023	Sequence 232023, A
	35	60.0	598	14	US-10-027-632-232023	Sequence 232023, A
	36	60.0	621	13	US-10-027-632-258272	Sequence 258272, A
	37	60.0	621	14	US-10-027-632-258272	Sequence 258272, A
	38	60.0	629	13	US-10-027-632-236107	Sequence 236107, A
	39	60.0	629	14	US-10-027-632-236107	Sequence 236107, A
	40	60.0	653	13	US-10-027-632-23519	Sequence 23519, A
	41	60.0	653	13	US-10-027-632-23520	Sequence 23520, A
	42	60.0	653	13	US-10-027-632-23521	Sequence 23521, A
	43	60.0	653	13	US-10-027-632-23522	Sequence 23522, A
	44	60.0	653	14	US-10-027-632-23519	Sequence 23519, A
	45	60.0	653	14	US-10-027-632-23520	Sequence 23520, A

ALIGNMENTS

RESULT 1

US-09-784-423-125

Sequence 125, Application US/09784423

Patent No. US20020012924A1

GENERAL INFORMATION:

APPLICANT: Schumm, James W.

Bacher, Jeffery W.

TITLE OF INVENTION: MATERIALS AND METHODS FOR

IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Promega Corporation

STREET: 2800 Woods Hollow Road

CITY: Madison

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53711-5399

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

COMPUTER: IBM compatible PC

OPERATING SYSTEM: Windows 95

SOFTWARE: Word 97 (DOS text format)

CURRENT APPLICATION DATA: US/09/784,423

APPLICATION NUMBER: 15-Feb-2001

FILING DATE: 15-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/018,584

FILING DATE: 04-Feb-1998

ATTORNEY/AGENT INFORMATION:

NAME: Grady J. Frenchick

REGISTRATION NUMBER: 29,018

REFERENCE/DOCKET NUMBER: 16026.9180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 257-3501

TELEFAX: (608) 257-2275

INFORMATION FOR SEQ ID NO: 125

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 25
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 125
US-09-784-423-125

Query Match      100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
DB 1 TGTGCCAGGACCAAGAAATTACAG 25

RESULT 2
US-09-784-423-32/c
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1000 bp
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Double
;   TOPOLOGY: Circular
;   MOLECULE TYPE: Genomic DNA
;   HYPOTHETICAL: no
;   IMMEDIATE SOURCE:
;   CLONE: S132
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT: 22
; SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      100.0%; Score 25; DB 9; Length 1000;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TGTGCCAGGACCAAGAAATTACAG 25
DB 726 TGTGCCAGGACCAAGAAATTACAG 702

RESULT 3
US-10-027-632-311837/c
; Sequence 311837, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311837
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-311837

Query Match      68.0%; Score 17; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAATTTA 22
DB 536 CAGGAACCAAGAAATTTA 520

RESULT 4
US-10-027-632-311837/c
; Sequence 311837, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 311837
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-311837

Query Match 68.0%; Score 17; DB 14; Length 624;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGACACGAGAAATTTA 22
Db 536 CAGGACACGAGAAATTTA 520

RESULT 5
US-10-017-161-1629/c
; Sequence 1629, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1629
; LENGTH: 7273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(7273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(264)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1125)..(1354)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1572)..(1721)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1955)..(2086)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3141)..(3257)
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; LOCATION: (4706)..(4858)
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US-10-017-161-1629
Query Match 68.0%; Score 17; DB 13; Length 7273;
Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3978 TGCCAGGACACCAAAAT 3962

RESULT 6
US-09-864-761-11479/c
; Sequence 11479, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 11479
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005961.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
US-09-864-761-11479

Query Match 64.0%; Score 16; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACACAGA 16
|||||
DB 226 TGTGCCAGGAACACAGA 211

RESULT 7

US-10-027-632-179918/c
; Sequence 179918, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179918
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-179918

Query Match 64.0%; Score 16; DB 13; Length 494;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACACAGA 16
|||||
DB 49 TGTGCCAGGAACACAGA 34

RESULT 8

US-10-027-632-179918/c
; Sequence 179918, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179918
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-179918

Query Match 64.0%; Score 16; DB 14; Length 494;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACACAGA 16
|||||
DB 49 TGTGCCAGGAACACAGA 34

RESULT 9

US-10-027-632-220234/c
; Sequence 220234, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220234
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220234

Query Match 64.0%; Score 16; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAATTTA 22
|||||
DB 357 AGGAACCAAGAAATTTA 342

RESULT 10

US-10-027-632-220235/c
; Sequence 220235, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006

```
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220235
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220235
```

```
Query Match 64.0%; Score 16; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 AGGAACCGAAGAAATTTA 22
|||||
Db 357 AGGAACCGAAGAAATTTA 342
```

```
RESULT 11
US-10-027-632-220234/c
; Sequence 220234, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220234
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220234
```

```
Query Match 64.0%; Score 16; DB 14; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 AGGAACCGAAGAAATTTA 22
|||||
Db 357 AGGAACCGAAGAAATTTA 342
```

```
RESULT 12
US-10-027-632-220235/c
```

```
; Sequence 220235, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220235
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220235
```

```
Query Match 64.0%; Score 16; DB 14; Length 624;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 AGGAACCGAAGAAATTTA 22
|||||
Db 357 AGGAACCGAAGAAATTTA 342
```

```
RESULT 13
US-10-027-632-114443
; Sequence 114443, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114443
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114443
```

```
Query Match 64.0%; Score 16; DB 13; Length 641;
```

Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCCAGGACCAGA 16
Db 227 TGTCCAGGACCAGA 242

RESULT 14
US-10-027-632-114443
; Sequence 114443, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114443
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114443

Query Match 64.0%; Score 16; DB 14; Length 641;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCCAGGACCAGA 16
Db 227 TGTCCAGGACCAGA 242

RESULT 15
US-10-027-632-253734/c
; Sequence 253734, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253734
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-253734

Query Match 64.0%; Score 16; DB 13; Length 1630;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCAGGACCAGAAATT 20
Db 898 CCAGGACCAGAAATT 883

Search completed: January 31, 2004, 17:39:49
Job time : 144 secs